

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 204874

TO: Gerald R Ewoldt

Location: rem/3C83/3C70

Art Unit: 1644

Friday, October 20, 2006

Case Serial Number: 10/620621

From: John DiNatale

Location: Biotech-Chem Library

REM-1B65

Phone: (571)272-2557

john.dinatale@uspto.gov

Search Notes

Examiner Ewoldt,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

John DiNatale Technical Information Specialist STIC Biotech/Chem Library (571)272-2557



77452

Searcher Phone:___

Date completed:____

Online Time:_

Searcher Prep Time:_

Date Searcher Picked up:___

STIC-Biotech/ChemLib

10-755

204874

STN:_

DIALOG:_______QUESTEL/ORBIT:_

Other (Specify):__

SEQUENCE SYSTEM: WWW/Internet:

LEXIS/NEXIS:

Sent: To: Subject:	R Ewo	in, Christina sday, October 17, 2 oldt, Gerald; STIC-B RUSH Seq Search	iotech/Chem	Lib	
Please rush.	Thanks Chris		10	a 20	
Chris Chan TC 1600 New (571)-272-0841 Remsen, 3E89	Hire Training Coordi	nator and SPE 1644	2	20	· • · · · ·
Original From: Sent: To: Subject:	Message Ewoldt, Gerald Tuesday, October 17, 2006 Chan, Christina RUSH Seq Search for 10/62		4	19 18	
Christina Please a	a; uthorize a RUSH S	earch.	6 da	20	
Thanks, G.R. Ewo Primary	ldt, Ph.D. Examiner ldg., <u>3C83</u>	1-10 including int	7 aa 8 9	20	r copy.
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NA#_____ AA#:_

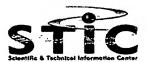
S/L:____ Oligomer:_

Inventor:____Litigation:__

_Text:

Encode/Transl:

Structure #:__



STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor 571-272-2507 Remsen 1 A51

VOI	untary results reedback rolling
>	I am an examiner in Workgroup: Example: 1610
>	Relevant prior art found, search results used as follows:
	☐ 102 rejection
	☐ 103 rejection
	Cited as being of interest.
	Helped examiner better understand the invention.
	Helped examiner better understand the state of the art in their technology.
	Types of relevant prior art found:
	☐ Foreign Patent(s)
	 Non-Patent Literature (journal articles, conference proceedings, new product announcements etc.)
>	Relevant prior art not found:
	Results verified the lack of relevant prior art (helped determine patentability).
	Results were not useful in determining patentability or understanding the invention.
Cor	mments:

Drop off or send completed forms to STIC/Biotech-Chem Library Remsen Bldg.



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GenCore version 5.1.9
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                    Copyright
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protein search, using sw model OM protein

October 18, 2006, 19:10:59 Run on:

; Search time 93.299 Seconds (without alignments) 98.011 Million cell updates/sec

US-10-620-621-1 85

1 TGYYXXXXXQSPEKSLEWIG 20 score: Sequence: Perfect

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2589679 segs, 457216429 residues Searched:

2589679 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqn1980s:* geneseqn1990s:* geneseqn2000s:* geneseqn2001s:* geneseqn2002s:* geneseqn2003as:* geneseqp2003bs:* geneseqp2004s:* A_Geneseq_8:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2006s:* geneseqp2005s:*

Aaw05034 Synthetic Aae27944 Murine 5G Adf70140 Anti-idio Adf70140 Anti-idio Adf70140 Anti-idio Adf5093 Variable Abp45615 Human BL Adg96442 Single ch Add7845 Human BL Add281037 Amino aci Add28121 Lymphoma Adz8121 Lymphoma Abp58454 Engineere Aef80925 Staphyloc Au81275 Human trk Abr55799 Heavy cha Abr55823 Heavy cha Abr55823 Heavy cha Abr55823 Heavy cha Abr41992 Ig H chan imm Adx41992 Ig H chan Aaw05029 Synthetic Adr14727 Amino aci Description ADM72027 AEF50993 ADZ51037 ADZ51043 ADD28121 ABP58454 AEF80925 AAU81275 AAW05034 AAE27944 ADF70140 ADR14717 ADG96442 AED78495 AAW05029 ADR14727 ABP45615 ABR55799 ABR55823 8 8 10 7 7 10 DB Length 470 255 255 255 467 470 Query Match 1 Score Result Š

Aed78511 Human B L	_	Adu72224 Signal pe	Adz73215 Human inc	Add28117 Lymphoma	Aar79244 Heavy cha	Aab50793 Murine an	Aea34944 Human ant		Aea42985 EphA2 ant	Aef10097 Mouse-hum	Aef10112 Mouse-hum	Aae03752 Murine PS	Adh44153 Human ant	Aeb21865 Human DC-	Aeb21868 Human DC-	Aeb21864 Human DC-	Aeb21869 Human DC-	Aeb21863 Human DC-	Aay87655 Murine PI	Abu08927 Mouse amy	Aay64689 Human 5'
AED78511	AAY64660	ADU72224	ADZ73215	ADD28117	AAR79244	AAB50793	AEA34944	AEB17185	AEA42985	0 AEF10097	0 AEF10112	AAE03752	ADH44153	AEB21865	AEB21868	AEB21864	AEB21869	AEB21863	AAY87655	ABU08927	AAY64689
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24	25	56	27	28	. 53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

SLE; systemic lupus erythematosus; autoimmune disease; monoclonal; anti-DNA antibody; CDR; complementarity determining region; 16/6 Id; idiotype; nuclear antigen. Synthetic peptide for treating systemic lupus erythematosus. Arg Glu, 'label= Met, Ala, Val Location/Qualifiers Asp, AAW05029 standard; peptide; 20 AA label= Trp, Ala 'label= Gln, 29-MAY-1997 (first entry) Misc-difference Misc-difference Misc-difference Misc-difference Synthetic. AAW05029; AAW05029

Ala /label= Lys, Glu, 'label= Val, Ser Misc-difference

WO9630057-A1

96WO-US004206 27-MAR-1996; 03-OCT-1996

(YEDA) YEDA RES & DEV CO LTD. (RYCU/) RYCUS A.

95IL-00113159.

28-MAR-1995;

Mozes E, Waisman A;

WPI; 1996-455014/45.

ADY96947 ADZ41992 ABP45631 ADG96458

New synthetic peptide(s) for treating systemic lupus erythematosus based on complementarity determining region of pathogenic anti-DNA monoclonal antibody that induces SLE-like disease in mice.

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Matches
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                        AAW05029-W05038 are synthetic peptides based on the complementarity-determining region (CDR) of the heavy or light chain of a pathogenic 16/6 Id anti-DNA monoclonal antibody (MAb), that induces a systemic lupus erythematosus (SLE)-like disease in mice. The peptides and their derivatives are used for treating SLE. The peptides inhibit or suppress specific antigen responses of SLE patients without affecting all other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pharmaceutical composition for treating systemic lupus erythematosus (SLE), has salt of peptide corresponding to complementarity-determining region of heavy/light_chain of anti-DNA 16/6 Id antibody that induces
                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                 complementarity determining region; CDR; heavy chain; light chain; monoclonal anti-DNA 16/6 idiotype antibody; l6/6 Id antibody; anti-DNA antibody; induces systemic lupus erythematosus; SLE.
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                                                                                                               Length 20;
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                                                                                                                                                                                                                                                                  Amino acid sequence of a peptide used to treat SLE.
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                                                                                                          94.1%; Sco...
100.0%; Pred. No. ...
0; Mismatches
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         Claim 3; Page 36; 51pp; English.
                                                                                                                                                                                                              ADR14727 standard; peptide; 20
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TEVA PHARM USA
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                                                                             immune responses
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                                                                                               Sequence 20 AA;
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Best Local &
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(TEVA-)
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The specification describes a pharmaceutical composition, comprising

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salt of a peptide with 12-30 consecutive amino acids having a sequence corresponding to an amino acid sequence found within complementarity-determining region (CDR) of the heavy or light chain of the human monoclonal anti-DNA 16/6 idiotype (16/6 Id) antibody, or a heavy or light chain of a pathogenic anti-DNA monoclonal antibody that induces systemic lupus erythematosus (SLE)-like disease response in mice. The composition is useful for treating SLE and for alleviating symptoms of SLE in a human subject. The present sequence represents a peptide which is used in pharmaccutical compositions of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16/6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New synthetic peptide(s) for treating systemic lupus erythematosus based on complementarity determining region of pathogenic anti-DNA monoclonal antibody that induces SLE-like disease in mice.
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100.0%; Pred. No. 6.9e-07;
iive 0; Mismatches 0;
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Pred. No. 1e-06;
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                                                                                                                                                                                                                                                                                                                                                    similarity 100.
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Best Local Similarity
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22-MAY-2003; 2003WO-IL000424.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the present invention.
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                                                                                                                                                                                                           Shoenfeld Y;
                                                                                                                                                                                                                               WPI; 2004-042771/04.
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                                                                                                      WO2003099868-A2
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                                                                                                                                                                                                                                                                                   pooled plasma
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                                                                                 Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a synthetic peptide selected from a peptide of 12-30 amino acid residues with a sequence of, or found within, a complementarity-determining region (CDR) on the variable heavy (WH) or light (VL) chain of human monoclonal anti-DNA 16/61d antibody (hCDR). The composition comprising the peptide is useful for the treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 systemic lupus erythematosus (SLE) and amelioration of the clinical manifestations of the disease, particularly by modulating SLE-associated responses. The present sequence is murine mAb VH chain CDR peptide
                                                                                                                                             Complementarity-determining region; CDR; variable heavy chain; VH; VL; variable light chain; SLE-associated response; immunosuppressive; SLE; systemic lupus erythematosus; dermatological; therapy; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                New synthetic peptide useful for treating and ameliorating the clinical manifestations of systemic lupus erythematosus (SLE) by modulating SLE-associated responses.
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autoimmune disease; immunoglobulin; anti-idiotypic antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92.9%; Score 79; DB 5; Length 20; 75.0%; Pred. No. 1e-06; ive 0; Mismatches 5; Indels
                                                                                                                         Murine 5G12 mAb VH chain CDR1 based peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anti-idiotype antibody related peptide.
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                                                            AAE27944 standard; peptide; 20 AA
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TGYYMQWVKQSPEKSLEWIG 20
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(YEDA ) YEDA RES & DEV CO LTD
                                                                                                                                                                                                                                                                                   26-FEB-2001; 2001IL-00141647.
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                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15; Conservative
                                                                                                                                                                                                                                                                                                                                                WPI; 2002-698624/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20 AA;
                                                                                                                                                                                                                     WO200267848-A2
                                                                                                      27-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-FEB-2004
                                                                                                                                                                                                                                          06-SEP-2002
                                                                                  AAE27944;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADF70140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                           Mozes E;
                                                                                                                                                                                                   Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                   셤
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The present invention describes a method (M1) for identifying molecules (I) which mimic an idiotype of an autoimmune disease-associated autoantibodies in M1 comprises purifying autoantibodies from sera of one or more patients affilted with the autoimmune disease. binding the autoantibodies to a solid phase to form an affinity matrix, contacting pooled plasma or B cells comprising immunogalbulins with the affinity matrix followed by removal of unbound plasma components, eluting contacting pooled plasma or B cells comprising immunogalbulins with the affinity matrix followed by removal of unbound plasma components, eluting contracting the matrix, providing a molecular library comprising several molecule members, and contacting the anti-id with the molecular library and isolating the bound molecules which are bound by the anti-clay the bound molecules being molecules that mimic an idiotype of autoantibodies. (I) have immunosuppressive, antiinflammatory, dermatological, muscular, neuroprofective, CNS, antiinflammatory, chypertensive, endocrine, antipsoriatic, hepatotropic, virucide, antichyroid, thyromimetic, antiinfabetic, antiinfertility, antiinfermatic, antithrandic, neuroprofective, (NS, antiinfertility, antiinferminic, phthalmological, uropathic and antipyretic activities, and can be used in vaccines. The molecules (I), anti-Id and pharmaceutical compositions of the present invention can be used for treating an execution for screening chemical compounds for this potential use in treating antimental compounds for this potential use in the exemplification autoimmune disease. The present sequence is given in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying molecules, which mimic an idiotype of an autoimmune disease-associated autoantibody, useful for treating an autoimmune disease, e.g. myasthenia gravis, comprises the use of immunoglobulins purified from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
immunosuppressive, antiinflammatory; dermatological; muscular; neuroprotective; CNS; anti-Hy, nociropic; neurologitic; antithyroid; thyromimetic; antidabetic; anabolic; hypertensive; endocrine; antipsoriatic; hepatotropic; virucide; antianaemic; haemostatic; gastrointestinal; antiuloer; antimhertility; antitheumatic; antiathritic; nephrotropic; antiaterility; antitheumatic; ophthalmological; uropathic; antipyretic; vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; Page 12; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADR14717 standard; peptide; 20 AA
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Tokita

Ito Y,

Ohizumi I,

Synthetic.

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The invention relates to an antibody against the N terminus of glypican (GPC3). The antiboduy can be used for causing cell disruption and can be uses as an anti-cancer agent. The present sequence represents a chimeric mouse-human antibody MIE07 heavy chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibody against the N terminus of glypican 3(GPC3) causes cell
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75.0%; Pred. No. 3.3e-05;
ive 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disruption and is useful as an anticancer agent
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Sugo I, Kawai S, Ishiguro T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 4; SEQ ID NO 12; 122pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                    Nakano K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AEF50993 standard; protein; 470
                                                                                                                                                                                                                         04-SEP-2003; 2003WO-JP011318.
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                                                                                                                                                                                                                                                                                                                                                        (CHUS ) CHUGAI SEIYAKU KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2006-110188/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-269573/25.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 470 AA;
                                                                                          WO2004022739-A1.
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Homo sapiens
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Tanaka M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AEF50993;
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                                 Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
AEF50993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The specification describes a pharmaceutical composition, comprising a salt of a peptide with 12-30 consecutive amino acids having a sequence corresponding to an amino acid sequence found within complementarity-determining region (CDR) of the heavy or light chain of the human monoclonal anti-DNA 16/6 idiotype (16/6 Id) antibody, or a heavy or light chain of a pathogenic anti-DNA monoclonal antibody, or a heavy or light chain of a pathogenic anti-DNA monoclonal antibody that induces systemic lupus erythematosus (SLE)-like disease response in mice. The composition is useful for treating SLE and for alleviating symptoms of SLE in a human subject. The present sequence represents a peptide based on CDR1 of the heavy chain V region of monoclonal antibody 5dl2. The 5dl2 monoclonal antibody was isolated from mice with experimental SLE, and was shown to bind DNA and bear the 16/6 Id. The present peptide is used in pharmaceutical compositions of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pharmaceutical composition for treating systemic lupus erythematosus (SLE), has salt of peptide corresponding to complementarity-determining region of heavy/light chain of anti-DNA 16/6 Id antibody that induces immune response to SLE.
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                                                                                                                                                  complementarity determining region; CDR; heavy chain; light chain; monoclonal anti-DNA 16/6 idiotype antibody; 16/6 Id antibody; anti-DNA antibody; induces systemic lupus erythematosus; SLE; antibody 5G12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Weinstein V, Gilbert A, Klinger E;
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                                                                                                Synthetic peptide based on VH CDR1 of monoclonal antibody 5G12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 79; DB 8; Length 20;
Pred. No. 1e-06;
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75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TEVA-) TEVA PHARM IND LTD.
(TEVA-) TEVA PHARM USA INC.
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Best Local Similarity
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                                 21-OCT-2004
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Gaps

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Indels

Length 470;

Novel anti-glypican 3 antibody having high complement dependent and antibody dependent cell-mediated cytotoxicity activity with respect to cell expressing glypican 3, useful as anticancer agent and as cell growth

GPC3; glypican 3; anti-GPC3 antibody; cell disruption; anti-cancer; cytostatic; M1E07.

Mus sp.

ADM72027;

SXXXXXXXXXX

RESULT 7

Matches

ઠે d Konishi H; Y;

Igawa T, Kinoshita

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                                              The new invention relates to an anti-glypican 3 (GPC3) antibody (A1)

Comprising a heavy chain variable region having CDR1 CDR2 and CDR3 and a Light Chain variable region having CDR1, CDR2 and CDR3. The antibody comprises complementarity determining regions (CDR9) of amino acid sequence selected from a number of sequences fully defined in the sequence from a number of sequences fully defined in the septiminary regions (CDR9) of amino acid comprising one or several amino acid substitutions, deletions, additions antibody (A2) having an activity equivalent to (A1) and having a sequence comprising one or several amino acid substitutions, deletions, additions and/or insertions in the sequence of (A1); polymuclectide (N1) encoding the heavy-chain variable region or light-chain variable region of (A1); cell growth inhibitor (I) comprising (A1) as an active ingredient; and anticancer agent (II), comprising (A1) as an active ingredient; and cell growth inhibitor. (II) is useful as an anticancer agent and as a cell growth inhibitor. (II) is useful as an anticancer agent and as a cell growth inhibitor. (I) is useful as an anticancer agent and as a cell growth inhibitor. (I) is useful as an anticancer agent and as a cell growth inhibitor. (I) is useful as an anticancer agent and as a cell growth inhibitor. (I) is useful as an anticancer agent and as a cell growth inhibitor. (I) is useful for diagnosing cancer. (A1) has CDC and ADC activity. The present sequence is a variable region of a murine anticancer glypican-3 antibody.
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Pred. No. 3.3e-05;
0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                         Disclosure; SEQ ID NO 24; 184pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC.
(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human BLyS binding scFv SEQ ID 1626.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABP45615 standard; protein; 255 AA
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                                                                                                                                                                                                                                                                                                                                                         92.9%;
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2001US-0276248P.
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25-MAY-2001; 2001US-0293499P.
                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 75.u-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                Sequence 470 AA;
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16-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-AUG-2002
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inhibitor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ruben
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This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell cumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cycostatic, immunosuppressive, immunostimulant, immunomodilatory, antirheumatic and antiALDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and tragments of the antibodies described in the method of
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Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B cell proliferation, differentiation; scFv; myasthenia gravis; multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia; carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective; antinflammatory; antiasthmatic; antiallergic; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 71; DB 5; Length 255;
Pred. No. 0.00045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Indels
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                                                                                                          Claim 1; Page 2343-2344; 3148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADG96442 standard; protein; 255 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-NOV-2001; 2001US-0331469P.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 255 AA;
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to B lymphocyte stimulator (BiryS). The BiryS gene has been mapped to chromosome 13934 and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single chain antibody molecules (scFvs) derived, preferably, from the variable heavy (DR3 region that immunospecifically bind to a polypeptide, or fragment thereof, of either human, murine, rat or monkey BiryS. The present invention refers to the use of such antibodies in various methods for the detection, diagnosis and prognosis of diseases related to the aberrant expression or inappropriate function of BivyS or its receptor. As such, these compositions are useful for identifying immune disorders cuch, these compositions are useful for identifying immune disorders including myasthenia gravis and multiple sclerosis, inflammatory disorders e.g. asthma and rheumatoid arthritis, infectious diseases such as AIDS and proliferative disorders including leukaemia, carcinoma and retivities such as antirheumatic, antiallergic and cytostatic. This activities such as antirheumatic, antiallergic and cytostatic. This cinvention. NOTE: The sequence data for this partent did not form part of the printed specification, but was obtained in electronic format the printed specification, but was obtained in electronic format chiractely from WIPO at ftp.wipo.int/pub/published pct_sequences.
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invention relates to novel antibodies that immunospecifically bind
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Antiallergic, Antimiorobial, Anti-HIV, Cytosetatic; B-lymphocyte;
antibody; autoimmune disease; b-cell lymphoma;
systemic lupus erythematosus; rheumatoid arthritis; immune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antiinflammatory; Dermatological; Immunosuppressive; Antirheumatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83.5%; Score 71; DB 7; Length 255; 65.0%; Pred. No. 0.00045; ive 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inflammation; infectious disease; hyperproliferation.
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16-MAR-2001; 2001US-0276548P.
21-MAR-2001; 2001US-027379P.
25-MAY-2001; 2001US-0293499P.
15-UNA-2001; 2001US-0389748.
16-NOV-2001; 2001US-0331469P.
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18-JUN-2004; 2004US-0580347P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13; Conservative
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Best Local Similarity
Matches 13; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (RUBE/) RUBEN S M.
(BARA/) BARASH S C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US2005255532-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 255 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-JUN-2000;
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BARASH S C.

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the invention traters to a novel antibouy that immunospecializatify bittobe to a B Lymphocyte Stimmlator protein. The protein comprises an amino acid sequence that is 85% identical to the VH domain of any one of the single-combined fragments (serve) of SEQ ID NOS. 1-2128, and/or an amino acid acid sequence that is at least 85% identical to the VL domain of any one of the screws of SEQ ID NOS. 1-2128. The invention further comprises: an isolated mucleic acid molecule encoding the antibody, an isolated cell line that expresses the antibody; a method for detecting the expression of a B Lymphocyte Stimulator protein; a method for diagnosing an autoimmune disease or a B cell cancer. The antibody is useful for detecting expression of B Lymphocyte Stimulator protein, and in diagnosing, treating, preventing, or ameliorating an autoimmune disease or a B cell cancer. The autoimmune disease or a B cell cancer. The autoimmune disease or a B cell cancer. C protein, and in diagnosing, treating, preventing, or ameliorating an carbinator or autoimmune disease or a B cell cancer. The autoimmune disease is systemic diagnosing, treating, and preventing immune disease; (e.g. multiple collupus erythematosus or rheumatoid arthritis. It can also be used for diagnosing, treating, and preventing immune diseases (e.g. autoimmune or allergic disorders), infeatious diseases (c.g. lymphoma). This sequence represents a single-chain variable fragment collymphoma, or his sequence represents a single-chain variable fragment collymphoma, or protein of the invention. Note: This sequence is not shown in the protein of the invention. It has been electronically downloaded from the USPTO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibody therapy; H4-1BB; CD137; IgG4; cytostatic; immunosuppressive; antiinflammatory; antimicrobial; gene therapy; T cell mediated autoimmune disease; cancer; neoplasm; autoimmune disease; inflammatory disease; infectious disease; heavy chain.
                                                                                                                                                               New antibodies that immunospecifically binds to B Lymphocyte Stimulator protein, useful for diagnosing, treating, or preventing autoimmune disease, e.g. systemic lupus erythematosus or rheumatoid arthritis, or B
                                                                                                                                                                                                                                                                                                                        invention relates to a novel antibody that immunospecifically binds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 71; DB 9; Length 255;
Pred. No. 0.00045;
1; Mismatches 6; Indels
                                                                                   Hilbert D;
                                                                                     Choi GH, Vaughan T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 1626; 240pp; English.
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Matches 13; Conservative
                                                                                     Ruben SM, Barash SC,
                                                                                                                             WPI; 2005-808635/82.
                 (VAUG/) VAUGHAN T.
(HILB/) HILBERT D.
(CHOI/) CHOI G H. (VAUG/) VAUGHAN T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 255 AA;
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                                                                                                                                                                                                                                         cell cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       website.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
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The specification describes fully human antibodies against human 4-1BB (CD137) (H4-1BB). These antibodies are especially IgG4 antibodies. Antibodies for human 4-1BB are useful as immuno-enhancers of an antitumor or anti-viral immune response, or as immunomodulators of T cell mediated autoimmune disease. They can also be used as diagnostic tools for the detection of H4-1BB in blood or tissues of patients with cancer, autoimmune, or other disease. The antibody can also be used for treating cancer (prostate cancer, melanoma, or epithelial cancer), autoimmune diseases (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus, or myasthenia gravis), inflammatory diseases, and infectious diseases. ADZ51041, ADZ51042, and ADZ51043 represent the coding strand, complementary strand, and encoded protein of a construct encoding the heavy chain of an antibody of the invention.
                                                                                                                                                                                                                                         New monoclonal antibody that specifically binds to 4-1BB comprises a
light chain variable region and a heavy chain variable region, useful
treating cancer, autoimmune diseases, inflammatory diseases, or
infectious diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B-cell; malignant; immunoglobulin; immunoglobulin variable region; Ig variable region; glycosylation site; lymphoma; B cell receptor; cytostatic; gene therapy; glycosylation inhibitor; non-Hodgkin's lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 71; DB 9; Length 4.v., Pred. No. 0.00088;
                                                                                                                                     Ganguly S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lymphoma related immunoglobulin variable region.
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                                                                                                                                     Santoro M,
                                                                                                                                                                                                                                                                                                                                                                    Example 1; SEQ ID NO 9; 92pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADD28121 standard; protein; 97 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49 SGYYWSWIRQSPEKGLEWIG 68
                                                                                       (BRIM ) BRISTOL-MYERS SQUIBB CO.
                     10-OCT-2003; 2003US-0510193P. 08-OCT-2004; 2004US-00961567.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-MAR-2002; 2002GB-00005395.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-FEB-2003; 2003WO-GB000783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 65.v.,
Best Local 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JAN-2004 (first entry)
                                                                                                                                     Hefta LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stevenson F;
                                                                                                                                                                               2005-296269/30
                                                                                                                                                                                                          N-PSDB; ADZ51041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 470 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2003074059-A2.
                                                                                                                                     Jure-Kunkel M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-SEP-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADD28121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhu D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
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                                                                                                                                                                                                                                                                                                                                        New monoclonal antibody that specifically binds to 4-1BB comprises a light chain variable region and a heavy chain variable region, useful for treating cancer, autoimmune diseases, inflammatory diseases, or infectious diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The specification describes fully human antibodies against human 4-1BB (CD137) (144-1BB). These antibodies are especially 1gG4 antibodies. Antibodies for human 4-1BB are useful as immuno-enhancers of an antitumor or anti-viral immune response, or as immunomodulators of T cell mediated autoimmune disease. They can also be used as diagnostic tools for the detection of 14-1BB in blood or tissues of patients with cancer, autoimmune, or other disease. The antibody can also be used for treating cancer (prostate cancer, melanoma, or epithelial cancer), autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibody therapy; H4-1BB; CD137; IgG4; cytostatic; immunosuppressive; antiinflammatory; antimicrobial; gene therapy; T cell mediated autoimmune disease; cancer; neoplasm; autoimmune disease; inflammatory disease; infectious disease; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diseases (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus, or myaethenia gravis), inflammatory diseases, and infectious diseases. ADZ51035, ADZ51036, and ADZ51037 represent the coding strand, complementary strand, and encoded protein of a plasmid. This plasmid encodes the heavy chain of an antibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid sequence of heavy chain of anti-H4-1BB antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 83.5%; Score 71; DB 9; Length 467; Best Local Similarity 65.0%; Pred. No. 0.00087; Matches 13; Conservative 1; Mismatches 6; Indels
                                                                                                                                                                                                                               Ganguly S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .19
/note= "leader peptide"
                                                                                                                                                                                                                             Jure-Kunkel M, Hefta LJ, Santoro M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; SEQ ID NO 3; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADZ51043 standard; protein; 470 AA
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                                                                                                                                                                               (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                12-OCT-2004; 2004WO-US033587.
                                                                                                           10-OCT-2003; 2003US-0510193P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-OCT-2004; 2004WO-US033587.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                          2005-296269/30.
                                                                                                                                                                                                                                                                                               N-PSDB; ADZ51035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 467 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2005035584-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JUN-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
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Peptide

RESULT 13 ADZ51043

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Gaps

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Length 470;

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                                                                                                                                 presence of a glycosylation site; and (c) classifying the cell as malignant or normal on the basis of the presence or absence of a glycosylation site. Also described: (1) treating a patient suffering from or at risk of having lymphoma; (2) screening for substances capable of inhibiting glycosylation of the Ig variable region of the B cell receptor; and (3) screening for substances (S) capable of inhibiting the interaction between lectins of the type found in the germinal centre and N-glycans found on the surface of Ig of lymphoma cells. (S) has eytostatic activity, and can be used in gene therapy, and as a glycosylation inhibitor. The method is useful in classifying a B-cell as malignant or normal. The glycosylation inhibitor is useful in preparing a medicament for treating non-Hodgkin's lymphoma. The present sequence represents an Ig variable region sequence which is used in the exemplification of the present invention.
                     Classifying a B-cell as malignant or normal by isolating a sequence representing an Ig variable region from the B cell, detecting the presence of a glycosylation site and classifying the cell as malignant or
                                                                                                                an
                                                                                                  The present invention describes a method for classifying a B-cell as malignant or normal comprising: (a) isolating a sequence representing a immunoglobulin (Ig) variable region from the B cell; (b) detecting the
                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Superantigen, staphylococcal enterotoxin; antibody; cancer; tumour; cytostatic; vaccine; human; SEA/E-120; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note= "wild-type His substituted by Pro"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gly"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "wild-type Arg substituted by Gly"
                                                                                                                                                                                                                                                                                                                                 Score 70; DB 7; Length 97;
Pred. No. 0.00024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "wild-type Ile substituted by Thr"
                                                                                                                                                                                                                                                                                                                                                       6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "wild-type Ser substituted by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note= "wild-type Val substituted by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "C242 constant heavy chain"
226. .458
note= "SEA/E-120"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "5T4 variable heavy chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Engineered superantigen for human cancer therapy.
                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABP58454 standard; protein; 672 AA
                                                                              Disclosure; Fig 4; 61pp; English
                                                                                                                                                                                                                                                                                                                                                                               2 GYYXXXXXQSPEKSLEWIG 20
                                                                                                                                                                                                                                                                                                                                                                                                    GYYWSWIROSPEKGLEWIG 49
                                                                                                                                                                                                                                                                                                                                 82.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-APR-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121. .222
                                                                                                                                                                                                                                                                                                                                                        13; Conservative
WPI; 2003-902720/82
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus sp.
Synthetic.
Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
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                                                                                                                                                                                                                                                                                                           Sequence 97 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABP58454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
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The present sequence is a conjugate of a bacterial superantigen and an antibody moiety, and has been designed to target and destroy cancer cals. The bacterial superantigen is SEAF120 (see also ABPS8455), which was derived from staphylococcal enterotoxin E (SEE) by the incorporation of the following amino acid substitutions to reduce seroreactivity whilst maintaining production levels and biological activity. R206, N21f, S246, R27K, K79E, K81E, K83S and D27S. SEAF120 was genetically fused to the Fab moiety of the tumour reactive antibody 574. Substitutions were made to the 5T4 sequence to obtain higher yields: in the heavy chain, H41F, S44G, 169T and V113G; and in the light chain, F10S, T45K, 163S, F73L, T77S, L78V and 1833. An expression vector comprising DNA encoding the conjugate can be used to transform host cells for recombinant production of the conjugate. The conjugate is useful for treating cancer, including cancer of the lung, breast, colon, kidney, pancreas, ovary, stomach, Conjugate for therapy, has bacterial superantigen with a region in T-cell receptor and four regions to determine binding to class II major histocompatibility complex, antibody to cancer associated cell surface structure. note= "wild-type Ser substituted by Gly" note= "wild-type Lys substituted by Glu" note= "wild-type Phe substituted by Leu" by Ala" note= "wild-type Asn substituted by Thr" note= "wild-type Phe substituted by Ser" note= "wild-type Thr substituted by Lys" note= "wild-type Ile substituted by Ser" "wild-type Arg substituted by note= "wild-type Lys substituted by note= "wild-type Lys substituted by note= "wild-type Leu substituted by note= "wild-type Thr substituted by 566. .672 /note= "C242 constant light chain" B; note= "wild-type Lys substituted note= "wild-type Asp substituted 'note= "wild-type Leu substituted 459. .565 /note= "5T4 variable light chain" Walse Forsberg G, Erlandsson E, Antonsson P, Claim 12; Fig 10; 102pp; English. 19-JUN-2002; 2002WO-SE001188 28-JUN-2001; 2001SE-00002327. (ACTI-) ACTIVE BIOTECH AB note= WPI; 2003-201467/19. Misc-difference 246 Misc-difference 452 Misc-difference 469 Misc-difference 522 Misc-difference 252 Misc-difference 536 Misc-difference 542 Misc-difference 537 Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference WO2003002143-A1 09-JAN-2003 Region

Sequence 672 AA

Query Match

Bo.0%; Score 68; DB 6; Length 672;
Best Local Similarity 65.0%; Pred. No. 0.0044;
Matches 13; Conservative 0; Mismatches 7; Indels 0; Gaps

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1 TGYXXXXXQSPEKSLEWIG 20 |||| || || || || || 30 TGYYMHWVKQSPGKGLEWIG 49

g

Search completed: October 18, 2006, 19:26:43 Job time : 95.299 secs

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5.1.9
Biocceleration Ltd.
 version :
GenCore (c) 1993
         Copyright
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OM protein - protein search, using sw model

October 18, 2006, 19:27:25; Search time 13.299 Seconds (without alignments) 144.698 Million cell updates/sec Run on:

US-10-620-621-1 85 1 TGYYXXXXXQSPEKSLEWIG 20

Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

PIR 80:* Database :

pir1:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

68	Ig heavy chain V r	Ig heavy chain V r	g heavy	g heavy chain V	ש	g heavy chain V-	g heavy	g heavy chain	g heavy	g heavy	g heavy	g heavy chain V	Ig heavy chain V r	g mu chain - hum	g heavy	g heavy chain V	g heavy	heavy	g heavy	g heavy	g heavy chain	g heavy chain	g heavy chain	g heavy chain	g heavy	heavy	g heavy	g heavy	Ig heavy chain V r
ID	PH0978	S26320	PH0977	A49982	D2HUWA	S57464	A31933	S13689	S26898	S26806	S26805	S14474	S17604	S37454	S13688	S13687	S13686	S13685	S26319	JL0047	S47010	PS0057	S78052	A49045	F34964	S26912	S26938	S26902	S12421
DB	2	~	~	~	н	~	7	~	~	~						~	~	7	7	~	~	7	~	~	~	~	~	~	7
% Query Match Length	105	107	108	120	129	115	136	91	97	97	97	97	86	106	110	111	112	112	114	122	126	135	140	140	98	86	98	98	86
% Query Match	92.9	•	74.1	4.	٠	÷.	9.07	σ			o	σ			69.4	69.4	σ	69.4							68.2	68.2	68.2	æ	æ
Score	79	63	63	63	62	61	9	29	29	59	20	29	50	59	29	59	59	59	29	29	59	50	29	50	28	28	28	28	29
Result No.	1	7	ო	4	<u>.</u>	9	7	æ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

Ig heavy chain V r		Ig mu chain - huma			Ig heavy chain V r	anti-Sm antibody V	Ig heavy chain pre	hypothetical hybri	Ig heavy chain V r						
S26801	S26807	869899	PH1668	PH1669	S37456	HVHU35	S18551	836265	830530	144151	S46393	849530	A34903	A24770	G2MSU1
7	~	~	~	7	7	н	~	~	7	~	~	7	7	~	-
66	66	104	109	110	116	117	117	118	123	126	129	135	137	140	117
68.2	68.2	68.2	68.2	68.2	68.2	68.2	68.2	68.2	68.2	68.2	68.2	68.2	68.2	68.2	67.1
28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	57
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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In John Park Chain V region (clone 178.166) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH0978
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH0978
A;Accession: PH0978
A;Accession: PH0978
A;Residues: 11-105 anti-DNA
A;Residues: 11-105 anti-DNA
A;Residues: UNIPARC:UPI0000176ACA
A;Coss-references: UNIPARC:UPI0000176ACA
A;Coss-references: UNIPARC:UPI0000176ACA
A;Experimental source: B cell, strain (NZB x NZW)PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
P;14-97/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92.9%; Score 79; DB 2; Length 105
75.0%; Pred. No. 7.7e-07;
iive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 92.9
Best Local Similarity 75.0
Matches 15, Conservative
RESULT 1
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Ig heavy chain V region - mouse C;Species: Mus musculus (house mouse) C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000 C;Accession: 826320 R;Stark, S.E.; Caton, A.J. J. Exp. Med. 174, 613-624, 1991 A;Title: Attibodies that are specific for a single amino acid interchange in a protein A;Reference number: 826309; MUID:91341421; PMID:1908510

A;Accession: S26320
A;Status: preliminary
A;Molecule type: mRMA
A;Residues: 1-107 «STA»
A;Cross-references: UNIPARC:UPI0000176ADF; EMBL:X59206
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
F;3-86/Domain: immunoglobulin homology <IMM>

Gaps ö 74.1%; Score 63; DB 2; Length 107; 65.0%; Pred. No. 0.00056; rive 0; Mismatches 7; Indels Query Match 74.1 Best Local Similarity 65.0 Matches 13; Conservative

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1 TGYYXXXXXQSPEKSLEWIG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TGYYXXXXQSPEKSLEWIG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32 TGYYWGWIRQPPGKGLEWIG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 YYXXXXXQSPEKSLEWIG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 71.8 Best Local Similarity 61.1 Matches 11, Conservative
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                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 60.0
Matches 12; Conservative
A; Molecule type: protein A; Residues: 1-129 <TAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: S57464
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                                                                                                              C, Genetics:
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Ig heavy chain V region (BA7.1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Beceis: Mus musculus (house mouse)
C;Becesion: A49982
R;Lin, C.; Kieber-Emmons, T.; Villalobos, A.P.; Foster, M.H.; Wahlgren, C.; Kleyman, T.R
J. Biol. Chem. 269, 2805-2813, 1994
A;Title: Topology of an amiloride-binding protein.
A;Reference number: A49982; MUID:94132051; PMID:8300613
A;Accession: A49982
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: L-120 cLINA
A;Residues: L-120 cLINA
A;Residues: L-120 cLINA
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <INMA
                                                                                                                                                                                         In heavy chain V region (clone 10-c1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH0977
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J; Exp. Med. 176, 761-779; 1992
A;Title: Both igM and igG anti-DNA antibodies are the products of clonally selective B A;Title: Both igM and igG anti-DNA antibodies are the products of clonally selective B A;Accession: PH0971; MUID:92181444; PMID:1512540
A;Accession: PH0971; MUID:9218144; PMID:1512540
A;Accession: PH0971; MUID:9218144; PMID:1512540
A;Ccostion: PH0971; MUID:9218144; PMID:1512540
A;Ccost-references: UNIPARC:UPIO000176AC9
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superimental source: B cell, strain [NZB x NZW]F1
C;Superimental source: B cell, strain [NZB x NZW]F1
C;Superimental immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology < NTM>
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: A02099
R;Takahashi, N.; Tetaert, D.; Debuire, B.; Lin, L.C.; Putnam, F.W.
Proc. Natl. Acad. Sci. U.S.A. 79, 2850-2854, 1982
A;Title: Complete amino acid sequence of the delta heavy chain of human immunoglobulin A;Reference number: A02099; MUID:82222225; PMID:6806818
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                                     18 TGYYMHWVKOSHVKSLEWIG 37
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R;Paterson, G.; Wilson, G.; Kennedy, P.G.E.; Willison, H.J.
submitted to the EMBL Data Library, June 1995
A;Description: Analysis of anti-GM1 ganglioside IgM antibodies cloned from motor neuropa
A;Reference number: S57408
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A;Reaidues: 1-115 <PAT>
A;Cross-references: UNIPARC:UP100001137AD; EMBL:X87897; NID:g871273; PIDN:CAA61148.1; Pi
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C; Species: Xenopus laevis (African clawed frog)
C; Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C; Accession: A31933
R; Schwager, J.; Mikoryak, C.A.; Steiner, L.A.
Proc. Natl. Acad. Sci. U.S.A. 85, 2245-2249, 1988
A; Title: Amino acid sequence of heavy chain from Xenopus laevis IgM deduced from CDNA A; Reference number: A94192; MUID:88176921; PMID:2451244
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C;Date: 10-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C;Accession: S57464
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A; Residues: 1-136 <SCH>
A; Residues: 1-136 <SCH>
A; Cross-references: UNIPROT: P20956; UNIPARC: UPI000012CED7
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heteroterramer; immunoglobulin
F; 32-114/ Domain: immunoglobulin homology <IMM>
                                                                                               A; Green GBB 1GHV@
A; Cross-references: GDB:128528; OMIM:147070
A; Map position: 14q32.33-14q32.33
C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heteroterzamer; immunoglobulin
F;15-99/Domain: immunoglobulin homology < IMM>
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-99/Domain: immunoglobulin homology <1MM>
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A;Cross-references: UNIPROT:P01824; UNIPARC:UPI000012CEEF
C;Comment: This chain was isolated from an IgD myeloma protein.
                                                                                                                                                                                                                                                                                                                                        Length 129;
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tive 0; Mismatches
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A,Cross-references: UNIPARC:UPI0000116488; EMBL:Z14242; NID:g37716; PIDN:CAA78611.1; PII
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <1MM>
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R;van Es, J.H.; Gmelig Meyling, F.H.J.; van de Akker, W.R.M.; Aanstoot, H.; Derksen, R.I. submitted to the EMBL Data Library, November 1990
A;Reference number: S14474
A;Accession: S14474
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A;Residues: 1-97 <ESJ>
A;Cross-references: UNIPARC:UPIO000115ECO; EMBL:X56591; NID:g37235; PIDN:CAA39929.1; PII
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
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C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
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C; Accession: $26806
R; Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
Bur. J. Immunol. 22, 1075-1082, 1995
A; Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.
A; Reference number: $26800; MUID:92201299; PMID:1348029
A; Accession: $26806
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-97 < WEN>
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R; Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
Bur. J. Immunol. 22, 1075-1082, 1992.
A; Title: Polymorphism of human immunoglobulin V(H) 4 germ-line genes.
A; Reference number: S26800; MUID:92201299; PMID:1348029
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Pred, No. 0.0026;
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A; Residues: 1-97 <WEN>
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8256898
19 heavy chain V region (clone DP-63, V(H)4.2) - human (fragment)
C;Species: Homo saplens (man)
C;Species: Homo saplens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26898: S12420
J, Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26898
A;Molecule type: DNA
A;Residues: 1-97 <TOM
A;Residues: 1-97 <
                                                                                                                                                                                                                                                                      Juneary chain V region - mouse (fragment)

If heavy chain V region - mouse (fragment)

C; Species: Mus musculus (house mouse)

C; Species: Mus musculus (house mouse)

C; Accession: 81368

R; Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H.

R; Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H.

A; Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to cl

A; Reference number: 813685; MUD:89338557; PMID:2503389

A; Accession: 813689

A; Accessi
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S26806
19 heavy chain V region - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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1 Similarity 55.0%; Pred. No. 0.0026;
11; Conservative 1; Mismatches 8; Indels
         1 TGYYXXXXQSPEKSLEWIG 20
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Gaps

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Length 110;

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A;Cross-references: UNIPARC:UP10000176904; EMBL:X53341
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;10-93/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                          Query Match 69.4%; Score 59; DB 2; Length 110
Best Local Similarity 55.0%; Pred. No. 0.0029;
Matches 11; Conservative 2; Mismatches 7; Indels
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S37454
Ig mu chain - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Decies: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: 337454
R;McIntosh, R.S.; Tandon, N.; Weetman, A.P.
submitted to the EMBL Data Library, September 1993
A;Beference number: 337454
A;Reference number: 337454
A;Status: preliminary
A;Molecule type: mRNA
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-106 cMCI-
A;Cross-references: UNIPARC:UPIO0001161BE; EMBL;X75022; NID:g404311; PIDN:CAA52930.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
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S13688
S13688
S19689
S19680
S1
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S17664
Ig heavy chain V region - mouse
S17664
Ig baces: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C; Accession: $17604
R; Clackson, T: Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A; Title: Making antibody fragments using phage display libraries.
A; Reference number: $17230; MUID:91326098; PMID:1907718
A; Accession: $17604
A; Residues: 1-98 cCLA>
A; Residues: 1-98 cCLA>
A; Residues: 1-98 cCLA>
C; Status: Teteferences: UNIPARC; UPI0000176D59
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Superfamily: immunoglobulin homology < IMM>
F; 8-91/Domain: immunoglobulin homology < IMM>
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         1 TGYYXXXXQSPEKSLEWIG 20
                                                             30 SGYYWSWIRQPPGKGLEWIG 49
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Matches 12, Conserv
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A; Molecule type: mRNA
A; Residues: 1-110 <PEN>
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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- permanent accession numbers. The new UniProt record may not contain the previous temporary numbers from the most recent version of UniProt. These sequences have been assigned new Please note that the curators of the UniProt database have purged some temporary accession
- extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein If you encounter an accession number from an older search run against UniProt (results file

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher. members of the public who may encounter UniProt temporary accession When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or

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                                                                                                                                                                                                                 11-0CT-2004, integrated into UniProtKB/TrEMBL.
11-0CT-2004, sequence version 1.
11-0CT-2006, sequence version 1.
11-0CT-2006, sequence version 10.
10.7-FEB-2006, entry version 10.
Ab 126.33 heavy chain variable and joining regions (Fragment).
Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Murinae; Mus
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21-DEC-2004, sequence version 1.
07-FEB-2006, entry version 8.
                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M74139; AAA3776.1; -; mRNA.
SMR; Q65ZR6; 18-134.
Ensembl; ENSMUSG00000057641; Mus musculus.
InterPro; IPR003599; 1G.
InterPro; IPR003109; 1G-like.
InterPro; IPR013106; V-set.
SMART; SM00409; IG; 1.
SMART; SM00409; IG; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin domain.
NOW TER.
SEQÜENCE 134 AA; 14908 MW; 1852D86D26FC75
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       Q6B6US_RABIT
Q6B6UG_RABIT
HV29 MÖUSE
Q920EB MÜUSE
HV57 MÕUSE
Q6B6U4_RABIT
HV35 MÕUSE
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NUCLEOTIDE SEQUENCE.
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Q6b6z2
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Q8wux4
Q6gmx5
Q9bqb8
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Q9u195
P01811
Q8izd7
Q4vab6
Q6b6z0
Q6b6s8
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Q96aa6
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        GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                      2849598 seqs, 925015592 residues
                                                                                                                                                                                                                                                                                                                                                                                                   Q65ZR6 MOUSE
Q5R3X0_MOUSE
Q95973_HUMAN
Q7TMK1_MOUSE
HV2F HUMAN
Q6B6Z2_RABIT
HV01_XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O9GYZZ MOUSE
O8WUX4 HUMAN
O6GMXS HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9BQBB HUMAN
Q9BU10 HUMAN
Q96AA6 HUMAN
Q7Z3Y6 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HV1G HUMAN
Q9UL94 HUMAN
Q9UL95 HUMAN
HV41 MÕUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HV41 MÖUSE
0812D7 HUNAN
0812D7 HUNAN
06820 RABIT
068713 RABIT
068713 RABIT
1817 MÖUSE
HV12 MÖUSE
HV17 MÖUSE
090XE9 MÖUSE
HV17 MÖUSE
090XE9 MÖUSE
HV17 MÖUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HV2I HUMAN
Q91WR1 MOUSE
                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                             - protein search, using sw model
                                                                                                                                                   Gapop 10.0 , Gapext 0.5
                                                                                                                       1 TGYYXXXXXOSPEKSLEWIG
                                                                                                                                                                                                                                                                           UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                                           seq length: 0
seq length: 200000000
                                                                                                   US-10-620-621-1
85
                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1117
1119
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483
                Copyright
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Match
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                                                                                                                Perfect score:
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Maximum DB
                                              OM protein
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Best Available Copy

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Gaps

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Length 134; 7; Indels

Gaps

us-10-620-621-1.rup

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunglobulin heavy chain variable region (Fragment).
Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Lagomorpha; Leporidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=15623575; DOI=10.1084/jem.20041849;
Rhee K.J., Jasper P.J., Sethupathi P., Shanmugam M., Lanning D.,
Knight K.L.;
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
3D-structure; Direct_protein sequencing; Immunoglobulin domain; Immunoglobulin V region.
CHAIN I >129 Ig heavy chain V-II region WAH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Positive selection of the peripheral B cell repertoire in gutassociated lymphoid tissues.";
J. Exp. Med. 201:55-62(2005).
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                                                                                                                 Ig heavy chain V-II region WAH.
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                                                                                                                                                                                                                                                          Score 62; DB 1; Length 123
Pred. No. 0.0067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                             14117 MW; D5D53D47ABE51319 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 AA; 10513 MW; 5D3FDC87553C9680 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-SEP-2004, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 AA
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                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
InterPro; IPR013106; V-set.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                 1 TGYYXXXXXQSPEKSLEWIG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 TGYYWGWIRQPPGKGLEWIG 51
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                                                                                                                                                                                                                                                                                     72.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 60.0
Marches 12; Conservative
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                129 1
129 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=New Zealand;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 RABIT
QGB6Z2 RABIT
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P20956;
                                                                                                                                                                                                NON TER
SEQUENCE
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SEQUENCE
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                                                                                                                                                                         DOMAIN
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                                                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein.
-!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN SEQUENCE.
MEDLINE=822225; PubMed=6806818;
Takahashi N., Tetaert D., Debuire B., Lin L.-C., Putnam F.W.;
"Complete amino acid sequence of the delta heavy chain of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 63; DB 2; Length 470;
Pred. No. 0.018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Indels
  Strausberg R.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
REQUENCE 470 AA; 51728 MW; 6D90E4DF896BB090 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986, integrated into UniProtXB/Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74.1%; Scc. 65.0%; Pred. No. v.. 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMR; P01824; 2-129.
SMR; P01824; 2-129.
GlycoSuiteDB; P01824; --.
GO; GO:0005576; C:extracellular region; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 AA.
                                                                                                                                                                                                                                               INCEPTO: IPRO01359; IG.
INCEPTO: IPRO01359; IG.
INCEPTO: IPRO0110; IG-like.
INCEPTO: IPRO01359; IG.
INCEPTO: IPRO01359; IG.
INCEPTO: IPRO01359; IG_MHC.
INCEPTO: IPRO13106; V-Sec.
PAM. PRO7554; CI-Sec: 3.
SMART; SMO0409; IG: 1.
SMART; SMO0407; IGC1, 2.
SMART; SMO0407; IGC1, 2.
PROSITE; PSO0290; IG_LIKE; 4.
PROSITE; PSO0290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                   BC055910; AAH55910.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-MAR-2006, entry version 36.
Ig heavy chain V-II region WAH.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003599; IG.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig.v.
InterPro; IPR013106; V-Set.
Pfam; PP07686; V-Set; 1.
SMART; SM00409; IG; 1.
                                                                                                                                                                                             HSSP; P01865; 1KB5.
MGI; MGI:2144790; AI324046.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 65.01
Conservative
13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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P01824;
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                       TISSUE=Lymph;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GHM protein.
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                                                                                                                                   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarnhini, Hominidae,
   "Nucleotide sequences of eight human natural autoantibody VH regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 69.4%; Score 59; DB 2; Length 595; Best Local Similarity 55.0%; Pred. No. 0.13; Matches 11; Conservative 1; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
SEQUENCE 595 AA, 65291 MW, 0D4B50776545714E CRC64;
                                reveals apparent restricted use of VH families.";
J. Immunol. 142:4054-4061(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-JUL-2004, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   597 AA.
                                                                                                                                                                                                                                                                                                       HSSP; P01861; 1ADQ.
SMR; Q8WUX4; 27-256.
Ensembl; ENSG0000130076; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50835; IG LIKE; 5.
PROSITE; PS00290; IG MHC; UNKNOWN_3.
                                                                                                                                                                                                                                       EMBL; BC019235; AAH19235.2; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QGGMXS_HUMAN PRELIMINARY; PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TGYYXXXXXQSPEKSLEWIG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56 SGYÝWSWIRQPPGKGĽEWIG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-JUL-2004, sequence version 1. 07-FEB-2006, entry version 17.
                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig cl.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig v.
InterPro; IPR013106; V-Set.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF07654; C1-set; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00409; IG; 1.
SMART; SM00407; IGc1; 3.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
                                                                                                                                                                                                                                                                           G34964; G34964.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IGHM protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Lymph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=IGHM
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Tissueberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausher R.D., Collins F.S., Wagner L., Shemen C.W., Schuler G.D.,
Antschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield X.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Generch A., Schein J.E., Jones S.J.M., Marra M.A.,
Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 0.13;
1; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Ensemble 
                                                                                                                       NIH MGC Project;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; BC073767; AAH73767.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QBOBB HUMAN PRELIMINARY; PRT;
QBBQBB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TGYYXXXXXQSPEKSLEWIG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 SGYYWSWIROPPGKGLEWIG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001, sequence version 1. 07-FEB-2006, entry version 27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 69.4%;
Best Local Similarity 55.0%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q6GMX5; 20-249.
NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE
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Bur. J. Immunol. 23:846-851(1993).
-1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
-1- SIMILARITY: Contains 1 Lonsortium, see http://www.uniprot.org/terms
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=93209281; PubMed=7681398;
Mariette X., Tsapis A., Brouet J.C.;
"Nucleotidic sequence analysis of the variable domains of four human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [GENOMIC DNA].
MEDILINE=88296408; PubMed=2841108;
Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
Ohno H., Fukuhara S., Honjo T.;
"Dispersed localization of D segments in the human immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           monoclonal IgM with an antibody activity to myelin-associated glycoprotein.";
                                                                                                                                                                                                                                                                                                                    68.2%; Score 58; DB 2; Length 116; 55.0%; Pred. No. 0.032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunoglobulin domain; Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                          116 AA; 12903 MW; CE3D8A846616C908 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1991, integrated into UniProtKB/Swiss-Prot. 01-NOV-1991, sequence version 1. 07-MAR-2006, entry version 36. Ig heavy chain V-I region V35 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X07448; -; NOT_ANNOTATED_CDS; Genomic_DNA.
PIR; S00476; HYMU35.
HSSP; P01751; LNQB.
SMR; P23083; 20-117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [2]
NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 20-116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 AA
                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO: 0005576; C: extracellular region; NAN GO; GO: 0003823; F: antigen binding; NAS. GO: 0000855; P: immune response; NAS. InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
InterPro; IPR013106; V.set.
Ffam, PF07686; V-set.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ensembl; ENSG00000130076; Homo sapiens.
LinkHub; P23083; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                   1 TGYYXXXXXQSPEKSLEWIG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                              30 SGYYWNWIRQPPGKGLEWIG 49
                   SMR; Q723Y6; 1-97.
InterPro; IPR003599; IG.
InterPro; IPR003196; Ig-like.
InterPro; IPR003596; Ig-v.
InterPro; IPR013106; V-set.
SMART; SM00409; IG; 1.
SMART; SM00409; IG; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            heavy-chain locus.";
EMBO J. 7:1047-1051(1988).
                                                                                                                                                                                                                                                                                                                                                                      11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                         116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
  HSSP; P18532; 1KCV.
                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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                                                                                                                                                                                                                                                       NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                         Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                  Neale G.A., Kitchingman G.R.; "mRNA transcripts initiating within the human immunoglobulin mu heavy chain enhancer region contain a non-translatable exon and are extremely heterogeneous at the 5' end."; Nucleic Acids Res. 19:2427-2433(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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Tinguely M., Rosenquist R., Sundstroem C., Amini R.M., Kuppers
Hansmann M.L., Brauninger A.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HISSP, PO1961, 1120.

SMR; Q96AA6; 27-256.

Ensembl; ENSGO0000130076; Homo sapiens.

InterPro; IPR001100; Ig-like.

InterPro; IPR003599; Ig c1.

InterPro; IPR003596; Ig-MHC.

InterPro; IPR013596; Ig-MHC.

InterPro; IPR013106; V-set.

PEnd; PP07654; C1-set; 4.

SMART; SM00407; IGC1; 3.

SMART; SM00407; IGC1; 3.

SMART; SM00406; IG; 1.

SMART; PS00299; IG MHC; UNKNOWN 3.

PROSITE; PS00299; IG MHC; UNKNOWN 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 625;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Indels
                                                                                                                                     NIH MGC Project;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69.4%; Score 59; DB 2;
55.0%; Pred. No. 0.14;
iive 1; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2003, integrated into UniProtKB/TrEMBL.
01-OCT-2003, sequence version 1.
07-FEB-2006, entry version 14.
Rearranged VH4-34 V gene segment (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q7Z3Y6_HUMAN PRELIMINARY; PRT; 116 AA.
Q7Z3Y6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AJ564425; CAD92032.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; BC017356; AAH17356.2; -; mRNA.
PIR; S15590; S15590.
                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
MEDLINE=91252286; PubMed=1904154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGYYWSWIRQPPGKGLEWIG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TGYYXXXXXOSPEKSLEWIG 20
                          mouse cDNA sequences.
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                                                                                          NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=VH4-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11;
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TYPE: amino acid
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RESULT 1
US-08-913-994B-1
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                                                                                           October 18, 2006, 19:45:04; Search time 24.1237 Seconds (without alignments) 72.568 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                                                                                                                                                                                                                              /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/HCOMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
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            5.1.9
Biocceleration Ltd
                                                                                                                                                                                                                                                                            650591
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US-08-913-994B-6

US-08-914-21

US-08-914-21

US-09-471-276-821

US-09-724-409-7

US-09-724-530-7

US-09-724-530-7

US-09-724-530-7

US-09-724-530-7

US-09-724-69-7

US-09-257-069-2

US-09-257-069-2

US-09-257-069-2

US-09-471-276-850

US-09-471-276-850

US-09-698-705-13

US-08-698-705-13

US-08-698-705-13

US-08-698-705-13

US-08-478-039-79

US-08-478-039-79

US-08-478-039-77

US-08-478-039-77

US-08-478-039-77

US-08-478-039-77

US-08-478-039-77

US-08-478-039-77

US-08-478-039-77
                                                                                                                                                                                                                                                                        hits satisfying chosen parameters:
                                                                                                                                                                                                                                                650591 seqs, 87530628 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
            GenCore version (c) 1993 - 2006
                                                                                                                                                                                                                                                                                                                                           Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                  - protein search, using sw model
                                                                                                                                                                            1 TGYYXXXXXQSPEKSLEWIG 20
                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                    Issued Patents AA:*
                                                                                                                                                                                                                                                                                                     length: 0
length: 2000000000
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85
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                                                                                                                                                                                                                                                                           Total number of
                                                                                                                                                                                                                                                                                                      sed
                                                                                                                                                                                                        Scoring table:
                                                                                                                                                               Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB
Maximum DB
                                                                  OM protein
                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                 Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL INFORMATION:
APPLICANT: MOZES, Edna
WALSMAN, ARI
TITLE OF INVENTION: SYNTHETIC PEPTIDES AND PHARMACEUTICAL
COMPOSITIONS COMPRISING THEM FOR THE TREATMENT
OF SYSTEMIC LUDUS ERVTHEMATOSUS (SLE)
                      Sequence
Sequence
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                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: United States of America

ZIP: 20001

COUNTRY: United States of America

ZIP: 20001

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC Compatible

COMPATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/913,994B

FILING DATE: 29-Sep-1997

PRIOR APPLICATION NUMBER: PCT/US96/04206

FILING DATE: 28-MAR-1995

ATTORNEY/AGENT INPORMATION:

MANY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSER: BROWDY AND NEIMARK
STREET: 624 Ninth Street N.W., Ste. 300
CITY: Washington
US-08-545-809A-118

US-09-726-219A-217

US-09-116-522-217

US-09-116-697-118

US-10-072-301A-36

US-10-072-301A-56

US-10-072-301A-56

US-08-793-450-4

US-08-793-768A-2

US-09-203-768A-2

US-09-203-768A-2

US-09-203-768A-2

US-09-203-768A-2

US-09-203-768A-2

US-09-10-301A-21

US-08-793-450-8

US-08-851-362D-19

US-08-851-362D-19

US-09-194-975-44

US-10-194-975-39

US-10-194-975-39

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US-10-194-975-39
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REGISTRATION NUMBER: 25,618
REGISTRATION NUMBER: 25,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2) 628-5197
737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08913994B; Patent No. 6613536; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide FEATURE:
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76.5%;
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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LENGTH: 128 amino acid
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                      CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Protein
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                               USA
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                                                                                                                                                                                                                                                                                                                                                                        AL INFORMATION:
APPLICANT: MOZES, Edna
WALSEMAN, ALI
TITLE OF INVENTION: SYNTHETIC PEPTIDES AND PHARMACEUTICAL
COMPOSITIONS COMPRISING THEM FOR THE TREATMENT
OF SYSTEMIC LUPUS ERYTHEMATOSUS (SLE)
                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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MEDIUM TYPES Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/913,994B

FILING DATE: 29-Sep-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/04206

FILING DATE: 27-MAR.1996

ATPLICATION NUMBER: IL 113,159

FILING DATE: 28-MAR.1995

ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, ROGET L.

REGISTRATION NUMBER: 25,618

ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, ROGET L.

REFERENCE/DOCKET NUMBER: MOZES=2
                                                                                                         94.1%; Score 80; DB 2; Length 20; 100.0%; Pred. No. 2e-07; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 92.9%; Score 79; DB 2; Length 20; Best Local Similarity 75.0%; Pred. No. 3.1e-07; Matches 15; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 20;
and Xaa in position 9 is Lys, Glu or Ala.
;
US-08-913-994B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 624 Ninth Street N.W., Ste. 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: D.C. COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
US-08-202-047-21
(**, Sequence 21, Application US/08202047
                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/08913994B
Patent No. 6613536
GENERAL INFORMATION:
                                                                                                                                                                                                              1 TGYYXXXXXQSPEKSLEWIG 20
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                                                                                      Query Match
Best Local Similarity 100.v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
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US-08-913-994B-6
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Gaps
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0
APPLICANT: CHESNUT, Robert W.
APPLICANT: CHESNUT, Robert W.
APPLICANT: POLLEY, Margaret J.
APPLICANT: POLLEY, James C.
APPLICANT: JONES, S. Tarran
APPLICANT: SALDANHA, Jose W.
APPLICANT: SALDANHA, Jose W.
APPLICANT: ALIDANHA, Antibodies to P-Selectin and Their Uses
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend And Townsend and Townsend and Townsend and Townsend ADDRESSEE: Townsend and Townsend ADDRESSEE: Tow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 21, Application US/08964690
Patent No. 6033667
GENERAL INFORMATION:
APPLICANT: CHESNUT, Robert W.
APPLICANT: POLLEY, Margaret J.
APPLICANT: JONES, S. Tarran
APPLICANT: SALDANHA, JOSE W.
APPLICANT: SALDANHA, JOSE W.
APPLICANT: APPLICANT: ALLANDON MARY M.
TITLE OF INVENTION: Antibodies to P-Selectin and Their Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000 CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 65; DB 1; Ler
Pred. No. 0.00075;
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OTHER INFORMATION: /label= MOUSE_IIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/202,047
FILLING DATE: 25-EB-1994
CLASSIFTCATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INPORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFRENCE/DOCKET NUMBER: 1413:
TELECOMMUNICATION INPORMATION:
TELEFONE: 415-326-240
INFORMATION FOR SEQ ID NO: 21:
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Query Match 74.1%; Score 63; DB 2; Length 93; Best Local Similarity 65.0%; Pred. No. 0.0012; Matches 13; Conservative 0; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                            49 TNYYWSXIRQSPGKGLEWIG 68
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| Sequence 81.2 Application US/09471276
| Patent No. 6822072
| GENERAL INFORMATION:
| APPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Ductort A. TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins. | TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins. |
| TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins. |
| TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins. |
| Patent No. 6822072 | 1992077 |
| FARLIER PRILING DATE: 1999-12-21 |
| EARLIER PILING DATE: 1999-04-09 |
| EARLIER PILING DATE: 1999-04-09 |
| SARLIER PILING DATE: 1999-04-09 |
| NUMBER OF SEQ ID NOS: 1622 |
| SOFTWARE: Patent.pm |
| SEQ ID NO 821 |
| LENGTH: 93 |
| LENGTH: 94 |
| LENGTH: 94 |
| LENGTH: 95 
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                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Patentin Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/964,690
FILING DATE:
CLASSIPICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/202,047
FILING DATE: 25-FEB-1994
ATTORNEY/AGENT INFRMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 14137-77
TELEFHONE: 415-326-2400
TELEFAX: 415-326-2400
TELEFAX:
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; OTHER INFORMATION: /label= MOUSE_IIA
US-08-964-690-21
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; NAME/KEY: SIGNAL
; LOCATION: -19..-1
US-09-471-276-821
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US-09-471-276-821
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US-08-388-366-8

Sequence 8, Application US/0888366

Sequence B. Septicant: Lopez, Osvaldo.

APPLICANT: Lopez, Dwane E. Septicant: Walner, Fred W. TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefore NURBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Merchant & Gould Server B. Se
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,366
FLING DATE: 03-JUL-1997
CLIASSIFICATION DATA:
APPLICATION NUMBER: US 08/187,407
FILING DATE: 12-DAN-1994
RRIGH APPLICATION NUMBER: US 07/990,542
FILING DATE: 14-DEC-1992
PRIOR APPLICATION NUMBER: US 07/493,299
FRICH APPLICATION NUMBER: US 07/324,392
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/324,392
FRIENG DATE: 14-MAR-1990
PRIOR APPLICATION NUMBER: US 07/324,392
FRIENG CAT'ET, CHAT'ES
NAME: CAT'ET, CHAT'ES
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 35,003
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US-09-724-409-7
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RESULT 11
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APPLICANT: Wall, Alan
APPLICANT: Wall, Alan
APPLICANT: Fall, H. Perry
TITLE OF INVENTION: RECOMBINANT ANTI-CD40 ANTIBODY AND USES THEREOF
FILE REFRENCE: 963-005
CURRENT APPLICATION NUMBER: US/09/724,530
CURRENT APPLICATION NUMBER: CRRENT APPLICATION NUMBER: US/09/328,296
PRIOR FILING DATE: CURRENT FILING DATE: 1999-06-08
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
LENGTH: 114
             Patent No. 683821
GENERAL INFORMATION:
APPLICANT: Siegall, Clay
APPLICANT: Francisco, Joseph
APPLICANT: FOR THE OF INVENTION: RECOMBINANT ANTI-CD40 ANTIBODY AND USES THEREOF
FILE REFERENCE: 9632-005
CURRENT APPLICATION NUMBER: US/09/724,409
CURRENT FILING DATE: 2000-11-28
PRIOR FILING DATE: 1999-06-08
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO
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Patent No. 6946129
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Siegall, Clay
APPLICANT: Wahl, Alan
APPLICANT: Francisco, Joseph
APPLICANT: Fell, H. Perry
ITILE OF INVENTION: RECOMBINANT ANTI-CD40 ANTIBODY AND USES THEREOF
FILE REPERENCE: 9632-005
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Pred. No. 0.0015;
0; Mismatches 7; Indels
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Application US/09724409
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74.1%;
Best Local Similarity 65.0%;
Matches 13; Conservative
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Best Local Similarity
Matches 13; Conserva
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US-09-328-296-7
                                                                                                                                                                                                                                                                                                                                                       LENGTH: 114
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APPLICANT: Koeppen, H.
APPLICANT: Lasky, L.
TITLE OF INVENTION: Anti-Tumor Antibody Compositions and Methods of Use
FILE REPERRICE: P177R1
CURRENT APPLICATION NUMBER: US/09/698,705
CURRENT FILING DATE: 2000-10-27
PRIOR FILING DATE: 1999-10-29
PRIOR PLING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 60/162,558
PRIOR APPLICATION NUMBER: US 60/182,872
PRIOR APPLICATION NUMBER: US 60/182,872
PRIOR SEQ ID NOS: 25
SEQ ID NO 8
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APPLICANT: Medical & Biological Laboratories Co.,Ltd.
APPLICANT: Medical & Biological Laboratories Co.,Ltd.
TITLE OF INVENTION: Monocload Antibody Specific for TITLE OF INVENTION: Phosphatidylinositol-3,4,5-Triphosphate; FILE REPERENCE: M3-008-US; CURRENT APPLICATION NUMBER: US/09/257,069; CURRENT APPLICATION NUMBER: UP 1998-252921; PRIOR FILING DATE: 1998-09-07; NUMBER OF SEQ ID NOS: 10; SOFTWARE: Patentin Ver. 2.0; SEQ ID NO 2; LENGTH: 124
                                                                                                                                                                                                          Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 121;
                                                                                                                                                                                             Score 63; DB 2; Length 113
Pred. No. 0.0015;
7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 63; DB 2; Length 121
Pred. No. 0.0016;
...----haa 7; Indels
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65.0%; Pred. No. v...
                                                                                                                                                                                                                                                      0; Mismatches
CURRENT APPLICATION NUMBER: US/09/328, 296
                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-698-705-8
Sequence 8, Application US/09698705
Patent No. 6824780
GENERAL INFORMATION:
APPLICANT: Devaux, B.
APPLICANT: Keller, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 TGYYIHWVKQSHGKSLEWIG 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09257069 Patent No. 6348580
                                                                                                                                                                                                                                                                                              1 TGYYXXXXQSPEKSLEWIG 20
                                                                                                                                                                                                                                                                                                                                       30 revilhwykoshekslewie 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGYYXXXXQSPEKSLEWIG 20
                 CURRENT FILING DATE: 1999-06-08
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
                                                                                                                                                                                                            Query Match
Best Local Similarity 65.0%;
Matches 13; Conservative
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Best Local Similarity 65.vv
The 13; Conservative
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                                                                                                                      ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-328-296-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-698-705-8
                                                                                                       LENGTH: 114
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APPLICANT: Lasky. L.
TITLE OF INVENTION: Anti-Tumor Antibody Compositions and Methods of Use
FILE REFERENCE: P1777H
FILE REPERENCE: P1777H
CURRENT APPLICATION NUMBER: US/09/698,705
CURRENT FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/162,558
PRIOR FILING DATE: 1999-10-29
PRIOR FILING DATE: 2000-02-16
NUMBER OF SEQ ID NOS: 25
SEQ ID NO 13
LENGTH: 222
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APPLICANT: SHIMAMURA, TOSHIRO
APPLICANT: HAMURA, JUNAI
APPLICANT: NAXAZAWA, HARUMI
APPLICANT: NAXAZAWA, YUKA
APPLICANT: SUGAMURA, KAZU
APPLICANT: SUGAMURA, KAZU
APPLICANT: TRESHITA, TOSHIKAZU
TITLE OF INVENTION: IMMUNOSUPPRESSANT
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS: 12
CORRESPONDENCE ADDRESS: 12
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 74.1%; Score 63; DB 2; Length 222; Best Local Similarity 65.0%; Pred. No. 0.0031; Matches 13; Conservative 0; Mismatches 7; Indels
  7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUS:
ADDRESSE: P.C.
STREET: 1.755 S. Jefferson Davis Highway, Suite 400
CITY: A-lington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: sequence is chimeric mouse/human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/230,843
  0; Mismatches
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21-APR-1994
                                                                                                                                                                                                                    ; Sequence 13, Application US/09698705
; Patent No. 6824780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TGYYXXXXQSPEKSLEWIG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 4, Application US/08230843; Patent No. 5582826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30 TGYYIHWVKQSHGKSLEWIG 49
                                               2 GYYXXXXXOSPEKSLEWIG 20
                                                                                               57 GYYWSWIROSPGKGLEWIG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial sequence
  12; Conservative
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                                                                                                                                                                                                                                                                                                                                            Koeppen, H.
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Keller, G.
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                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                              US-09-698-705-13
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US-08-230-843-4
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     Matches
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Sequence 850, Application US/09471276

Sequence 850, Application US/09471276

Sequence 850, Application US/09471276

Sequence 822072

APPLICANT: Duclert A.

APPLICANT: Duclert A.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

PATER REFERENCE: GENSET. 025CP1

CURRENT APPLICATION NUMBER: US/09/471,276

CURRENT FILING DATE: 1999-14-29

EARLIER FILING DATE: 1998-04-09

EARLIER FILING DATE: 1998-04-09

EARLIER FILING DATE: 1998-04-09

EARLIER FILING DATE: 1998-04-09

EARLIER FILING DATE: 1999-04-09

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EARLIER FILING DATE: 1999-04-09
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GENERAL INFORMATION:

APPLICANT: Medical & Biological Laboratories Co., Ltd.

TITLE OF INVENTION: Monoclonal Antibody Specific for

TITLE OF INVENTION: Monoclonal Antibody Specific for

TITLE OF INVENTION: Phosphatidylinositol-3,4,5-Triphosphate

FILE REFERENCE: M3-008-US

CURRENT APPLICATION NUMBER: US/10/007,790

CURRENT FILING DATE: 1999-02-24

PRIOR APPLICATION NUMBER: US/09/257,069

PRIOR APPLICATION NUMBER: US/09/257,069

PRIOR APPLICATION NUMBER: US/09/257,069

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2

LENGTH: 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 63; DB 2; Length 124;
Pred. No. 0.0016;
0; Mismatches 7; Indels
  Ouery Match 74.1%; Score 63; DB 2; Length 124; Best Local Similarity 65.0%; Pred. No. 0.0016; Matches 13; Conservative 0; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                 1 TGYYXXXXQSPEKSLEWIG 20
                                                                                                                                              30 TGYYMHWVKQSHGKSLEWIG 49
                                                                                                                                                                                                                                                                    Sequence 2, Application US/10007790 Patent No. 6818408
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Best Local Similarity 65.0%;
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
CORGANISM: Mus musculus
US-10-007-790-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patent.pm
SEQ ID NO 850
LENGTH: 140
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US-09-471-276-850
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                                                                                                                                                                                                                       RESULT 12
US-10-007-790-2
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## APPLICATION NUMBER: JP 094491/1993
### FILING DATE: 21-APR-1993
### FILING DATE: 21-APR-1993
### FILING DATE: 21-APR-1994
### FILING DATE: 07-MAR-1994
### ATTORNEY/AGENT INFORMATION:
### REGISTRATION NUMBER: 24,618
### REFERENCE/DOCKET NUMBER: 0010-0674-0X
### FILEPHONE: (703) 413-200
### OWNEY WAICH FILEPHONE: (703) ### FILEPHON
```

Search completed: October 18, 2006, 19:50:49 Job time : 25.1237 secs

us-10-620-621-1.rapbn

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GenCore version 5.1.9

Copyright (c) 1993 - 2006 Biocceleration Ltd.

On protein - protein search, using sw model

Run on: October 18, 2006, 20:43:15; Search time 14.3299 Seconds (without alignments)

112.851 Million cell updates/sec

112.851 Million cell updates/sec

Sequence: 1 TGYXXXXXQSPEKSLEWIG 20

Sequence: 2 Scoring table: BLOSUM62

Searched: 300827 seqs, 80857292 residues

Total number of hits satisfying chosen parameters: 300827

Minimum DB seq length: 0 00000000

Post-processing: Minimum Match 100%

Maximum Match 100%

Database: 1 FMC Celerra SIDS3/ptcdata/2/pubpaa/US09 NEW PUB.pep:*
2: / FMC Celerra SIDS3/ptcdata/2/pubpaa/US09 NEW PUB.pep:*
3: / FMC Celerra SIDS3/ptcdata/2/pubpaa/US08 NEW PUB.pep:*
3: / FMC Celerra SIDS3/ptcdata/2/pubpaa/US08 NEW PUB.pep:*
3: / FMC Celerra SIDS3/ptcdata/2/pubpaa/US08 NEW PUB.pep:*
3: / FMC Celerra SIDS3/ptcdata/2/pubpaa/US1 NEW PUB.pep:*
3: / FMC Celerra SIDS3/ptcdata/2/pubpaa/US1 NEW PUB.pep:*
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8: / FMC Celerra SIDS3/ptcdata/2/pubpaa/US1 NEW PUB.pep:*
8: / FMC Celerra SIDS3/ptcdata/2/pubpaa/US1 LWB PUB.pep:*
8: / FMC Celerra SIDS3/ptcdata/2/pubpaa/US1 LWB PUB.pep:*
8: / FMC Celerra SIDS3/ptcdata/2/pubpaa/US1 LWB PUB.pep:*
9: / FMC Celerra SIDS3/ptcdata/2/pubpaa/US1 LWB PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Appl	Appl	Appl	Appli	Appl	, Appli	Appli	Appli	0, Ap	Appli	, Appl	Appl	Appl	Appli	Appli	Appl	Appl	Appli	Appl						
ផ្គ	12,	12,		ω,	14,	4.	ģ	7	429	4,	85,	86,		ģ	1,	55,	•	7	33,		23,	35,	52,	64,	51,
Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence			Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
ΩΙ	US-10-526-741-12	1	US-11-221-902-18	US-11-221-902-8	US-11-221-902-14	-902	US-11-221-902-6	US-11-221-902-2	US-11-293-697-4290	US-10-972-296-4	US-09-784-950-85	US-09-784-950-86	US-09-784-950-87	-11-241-	US-11-111-688-1	US-11-111-688-55	US-11-094-132-67	US-11-413-563-2	US-09-784-950-33	US-09-784-950-31	US-09-784-950-23	US-11-267-860-35	US-11-221-902-52	US-11-221-902-64	US-10-981-300-51
DB	و	7	7	7	7	7	7	7	7	9	-	-	-	7	7		7	7	Н	Н	н	7	7	7	9
Length	470	470	120	447	139	447	447	450	491	117	78	92	92	116	124	126	128	139	190	202	205	16	96	98	118
% Query Match	92.9	92.9	75.3	75.3	74.1	74.1	74.1		71.8	70.6	69.4	69.4	69.4	69.4	69.4	69.4	69.4	69.4	69.4	69.4	69.4			68.2	•
Score	79	79	64	64	63	63	63	63	61		59						59								
Result No.		7	٣	4	S	y	7	60	σ	10	11	12	13	14	15	16	17							24	25

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Gaps

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Query Match 92.9%; Score 79; DB 6; Length 470; Best Local Similarity 75.0%; Pred. No. 4.1e-06; Matches 15; Conservative 0; Mismatches 5; Indels

8 8

US-11-414-676-12

Sequence 12, Application US/11414676

Publication No. US20060188510A1

GENERAL INFORMATION:

APPLICANT: ABURATANI, Hiroyuki

APPLICANT: MIDORIKAWA, Yutaka

APPLICANT: NAKANO, Kiyotaka

APPLICANT: OHIZUMI, IWAO

APPLICANT: ITO, Yukio

Sequence 19, Appl Sequence 21, Appl Sequence 82, Appl Sequence 82, Appl Sequence 110, Appl Sequence 110, Appl Sequence 13, Appl Sequence 14, Appl Sequence 67, Appl Sequence 10, Appl Sequence 10, Appl Sequence 12, Appl Sequence 12, Appl Sequence 84, Appl Sequence 84, Appl Sequence 86, Appl Sequence 46, Appl Sequence 46, Appl Sequence 46, Appl Sequence 46, Appl Sequence 53, Appl Sequence 53, Appl	-TERMINAL PEPTIDE OR C-TERMINAL Sequence: Mouse-human chain)
7 US-11-221-902-19 7 US-11-221-902-21 7 US-11-211-917-86 7 US-11-211-917-82 7 US-11-211-917-98 7 US-11-211-917-110 1 US-11-211-917-42 7 US-11-211-917-42 7 US-11-355-464-16 7 US-11-355-464-16 8 US-10-539-402-10 1 US-11-221-902-10 1 US-11-221-902-10 1 US-11-221-902-10 1 US-11-221-902-10 1 US-11-221-902-10 1 US-11-221-902-10 1 US-11-211-917-70 1 US-11-211-917-70 1 US-11-211-917-70 1 US-11-211-917-70 1 US-11-211-917-70 1 US-11-211-917-70	IGNMENTS T SOLUBLE N OD 26,741 08999 Artificial dy (MIE07 H
68.2 68.2 68.2 68.2 68.2 68.2 68.2 68.2	pplicat US200 ATTON: US200 ATTON: UDCRIKA AKANO, TO, YUK, TO, YUK, WITON: WITON: WITON: WITON: LE: CATION UDATE: LI NOS ATTON:
2 6 6 7 7 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	RESULT 1 US-10-526-741-12 ; Sequence 12, Applicati ; Publication No. US2006 GENERAL INFORMATION: ; APPLICANT: ABURATANI, APPLICANT: MIDORIKAW ; APPLICANT: ITO, YUK; APPLICANT: TOKITA, S TITLE OF INVENTION: TITLE OF INVENTION: FILE REFERENCE: CURRENT APPLICATION: FILE REFERENCE: CURRENT APPLICATION: FILE REFERENCE: PRIOR APPLICATION NUM PRIOR FILING DATE: 20 NUMBER OF SEQ ID NOS: SOFTWARE: PATORITION OF SEQ ID NOS: SOFTWARE: PATORITION: CURRENT APPLICATION NUM PRIOR FILING DATE: 20 NUMBER OF SEQ ID NOS: SOFTWARE: PATORITION: CURRENTH 470 TYPE: PRT COTHER INFORMATION: D OTHER INFORMATION: C

PEPTIDE

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US-11-221-902-14
US-11-221-902-14
Sequence 14, Application US/11221902
PUBLICATION NO. US20060088522A1
GENERAL INFORMATION:
APPLICATION: Wyeth
TITLE OF INVENTION: HUMANIZED ANTI-5T4 ANTIBODIES AND ANTI-5T4/CALICHEAMICIN CONJUGAT
FILE REFERENCE: 040000-0317285
CURRENT APPLICATION NUMBER: US/11/221, 902
CURRENT APPLICATION NUMBER: 2005-09-09
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PatentIn version 3.3
SEQ ID NO 14
LENGTH: 139
TYPE: PRT
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TITLE OF INVESTION: HUMANIZED ANTI-5T4 ANTIBODIES AND ANTI-5T4/CALICHEAMICIN CONJUGAT
FILE REFERENCE: 040000-0317285
CURRENT APPLICATION NUMBER: US/11/221,902
CURRENT FILING DATE: 2005-09-09
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin version 3.3
SEQ ID NO 4
                                                                                          OTHER INFORMATION: artificial sequence is derived from mouse and human antibody OTHER INFORMATION: sequences
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Pred. No. 0.0008;
0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                       Length 447;
                                                                                                                                                                                                                                                                                     Score 64; DB 7; Length 447
Pred. No. 0.0018;
1; Mismatches 7; Indels
                                                                                                                                                                 ; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(120)
; OTHER INFORWATION: heavy chain variable region
US-11-21-902-8
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OTHER INFORMATION: leader sequence
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Best Local Similarity 60.0%;
Matches 12; Conservative
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ORGANISM: Artificial
                                               ORGANISM: Artificial
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Best Local Similarity
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US-11-221-902-14
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US-11-221-902-4
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LENGTH: 447
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TITLE OF INVENTION: HUMANIZED ANTI-514 ANTIBODIES AND ANTI-514/CALICHEAMICIN CONJUGAT
FILE REFERENCE: 040000-0317285
CURRENT APPLICATION NUMBER: US/11/221,902
CURRENT APPLICATION NUMBER: US/11/221,902
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PATENTIN VETSION 3.3
SEQ ID NO 8
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TITLE OF INVENTION: HUMANIZED ANTI-5T4 ANTIBODIES AND ANTI-5T4/CALICHEAMICIN CONJUGAT
FILE REFERENCE: 040000-0311285
CURRENT APPLICATION NUMBER: US/11/221,902
CURRENT FILING DATE: 2005-09-09
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin version 3.3
SEQ ID NO 18
LENGTH: 120
APPLICANT: TOKITA, SUBUMU
TITLE OF INVENTION: ANTIBODY AGAINST SOLUBLE N-TERMINAL PEPTIDE OR C-TERMINAL PEPTIDE
TITLE OF INVENTION: PRESENT IN BLOOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) OTHER INFORMATION: artificial sequence is derived from mouse and human antibody ) OTHER INFORMATION: sequences US-11-221-902-18
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US-11-414-676-12
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Pred. No. 0.00046;
1; Mismatches 7; Indels
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                                                                                          CURRENT APPLICATION NUMBER: US/11/414,676
CURRENT FILING DATE: 2006-04-28
PRIOR APPLICATION UNBER: US/10/526,741
PRIOR FILING DATE: 2005-11-14
PRIOR FILING DATE: 2002-09-04
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18, Application US/11221902
Publication No. US20060088522A1
GENERAL INFORMATION:
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Publication No. US20060088522A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 60.0%;
Matches 12; Conservative
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ORGANISM: Artificial
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CURRENT APPLICATION NUMBER: US/10/972,296

CURRENT FILING DATE: 2004-10-25

PRIOR APPLICATION NUMBER: ep 98 11 35 95.7

PRIOR APPLICATION NUMBER: ep 98 11 35 95.7

PRIOR SEQ ID NOS: 22

SOFTWARE: Patentin version 3.2

SEQ ID NO 4
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                                         Score 63; DB 7; Length 450;
Pred. No. 0.0028;
0; Mismatches 7; Indels
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Pred. No. 0.0069;
                          74.1%; Sco. No. v. 65.0%; Pred. No. v. 0; Mismatches
                                                                                                                                                                                                                                                                   US-11-293-697-4290
; Sequence 4290, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICAAWT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT APPLICATION NUMBER: US/10/108,260
; PRIOR APPLICATION NUMBER: US/10/108,260
; RING RELING DATE: 2005-12-86
; NUMBER OF SEQ ID NOS: 5488
; SOFTWARE: PATENTIN USY: 2.1.
; SEQ ID NO 4290
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Publication No. US20060153833A1
GENERAL INFORMATION:
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Best Local Similarity 55.0<sup>3</sup>
Matches 11; Conservative
                                           Query Match
Best Local Similarity 65.0
Matches 13; Conservative
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; ORGANISM: Homo sapiens
US-11-293-697-4290
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US-10-972-296-4
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Best Local Similarity
US-11-221-902-2
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US-10-972-296-4
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Publication No. US2066088522A1
GENERAL INFORMATION:
APPLICANT: Wyeth
TITLE OF INVENTION: HUMANIZED ANTI-5T4 ANTIBODIES AND ANTI-5T4/CALICHEAMICIN CONJUGAT
TITLE OF INVENTION: HUMANIZED ANTI-5T4 ANTIBODIES AND ANTI-5T4/CALICHEAMICIN CONJUGAT
FILE REFERENCE: 040000-0317285
CURRENT APPLICATION WUMBER: US/11/221,902
CURRENT PILING DATE: 2005-09-09
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin version 3.3
SEQ ID NO 2
LENGTH: 450
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Sequence 6, Application US/11221902

Sequence 6, Application US/11221902

Sequence 6, Application US/11221902

Sequence 6, Application US/11221902

GENERAL INFORMATION:

APPLICANT: Wyeth

TITLE OF INVENTION: HUMANIZED ANTI-5T4 ANTIBODIES AND ANTI-5T4/CALICHEAMICIN CONJUGAT

FILE REFERENCE: 040000-0317285

CURRENT APPLICATION NUMBER: 2005-09-09

NUMBER OF SEQ ID NOS: 89

SOFTWARE: Patentin version 3.3

SEQ ID NO 6

LENGTH: 4477

TYPE: RRT
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OTHER INFORMATION: sequences
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         FEATURE:
NAME/KEY: MISC_FEATURE
D.CATION: (1)..(120)
OTHER INFORMATION: heavy chain variable region
US-11-221-902-4
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; LOCATION: (1)...(120)
; OTHER INFORMATION: heavy chain variable region
US-11-221-902-6
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NAME/KEY: MISC FEATURE
LOCATION: (1). (120)
OTHER INFORMATION: heavy chain variable region
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OTHER INFORMATION: sequences
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Best Local Similarity 65.03
Matches 13; Conservative
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APPLICANT: Yang, Alac-Dong
APPLICANT: Abgenix, Inc.
TITLE OF INVENTION: CINC.
FILE REPRENCE: Abx.-CBL/CD147
CURRENT APPLICATION NUMBER: US/09/784,950
CURRENT PILING DATE: 1090-03-03
PRIOR FILING DATE: 1990-03-03
PRIOR FILING DATE: 1998-03-03
SPRIOR FILING DATE: 1998-03-03
PRIOR FILING DATE: 1998-03-03
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TITLE OF INVENTION: METHOD OF TREATING CD30 POSITIVE LYMPHOWAS
FILE REFERENCE: MXI-327
CURRENT APPLICATION NUMBER: US/11/241,154
CURRENT FILING DATE: 2005-09-30
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Pred. No. 0.0027;
Pred. Transches 8; Indels
                                                                                                                                                                                                Score 59; DB 1; Length 92; Pred. No. 0.0027;
                                                                                                                                                                                                                                               8; Indels
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                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 87, Application US/09784950 Publication No. US20060104974A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-11-241-154-6
, Sequence 6, Application US/11241154
; Publication No. US20060177442A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                           1 TGYYXXXXQSPEKSLEWIG 20
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APPLICANT: Blacher, Russell W.
APPLICANT: Corvalan, Jose R.
APPLICANT: Culwell, Alan R.
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Ivanov, Vladimir E.
Lipani, John A.
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ilarity 55.0%;
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Best Local Similarity 55.0%;
Matches 11; Conservative
PRIOR FILING DATE: 1999-02-03
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Weber, Richard F.
                  NUMBER OF SEQ ID NOS: 105
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 86
LENGTH: 92
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Hales, Joanna
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CORGANISM: Homo sapiens
US-09-784-950-87
                                                                                                                               ; ORGANISM: Homo sapiens
US-09-784-950-86
                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                            11;
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LENGTH: 92
                                                                                                             TYPE: PRT
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Best Local
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APPLICANT: Liu, Oiang
APPLICANT: Weber, Richard F.
APPLICANT: Weber, Richard F.
APPLICANT: Abgenix, Inc.
TITLE OF INVENTION: CD147 BINDING MOLECULES AS THERAPEUTICS
FILE REFERENCE: ABX-CBL/CD147
CURRENT APPLICATION NUMBER: US/09/784,950
CURRENT FILING DATE: 2001-02-15
PRIOR PLING DATE: 1999-03-03
PRIOR APPLICATION NUMBER: 09/034,607
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Abgenix, Inc.
TITLE OF INVENTION: CD147 BINDING MOLECULES AS THERAPEUTICS
FILE REFERENCE: ABX-CBL/CD147
CURRENT APPLICATION NUMBER: US/09/784,950
CURRENT FILING DATE: 2001-02-15
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PRIOR FILING DATE: 1999-03-03
PRIOR APPLICATION NUMBER: 09/034,607
PRIOR APPLICATION NUMBER: 09/244,253
PRIOR FILING DATE: 1998-03-03
PRIOR FILING DATE: 1999-02-03
NUMBER OF SEQ ID NOS: 105
SEQ ID NO 85
LENGTH: 78
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PRIOR APPLICATION NUMBER: 09/244,253
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US-09-784-950-86
; Sequence 86, Application US/09784950
; Publication No. US20060104974A1
                                                              Sequence 85, Application US/09784950
Publication No. US20060104974A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                 Havrilla, Nancy
Ivanov, Vladimir E.
Lipani, John A.
Liu, Qiang
Weber, Richard F.
Yang, Xiao-Dong
                                                                                                                               APPLICANT: Davis, Geoffrey C.
APPLICANT: Blacher, Russell W.
COLVALIA, JOSE R.
APPLICANT: CUIWELL, AIR R.
                                                                                                                                                                                                                          Green, Larry L.
Hales, Joanna
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Best Local Similarity 55.0
Matches 11; Conservative
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; ORGANISM: Homo sapiens
US-09-784-950-85
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US-11-188-1

i Sequence 1, Application US/11111688

i Sequence 1, Application No. US20060115486A1

i GENERAL INFORMATION:
    GENERAL INFORMATION:
    APPLICANT: Pier, Gerald B
    APPLICANT: Relly-Quintos, Casie A
    APPLICANT: Cavacini, Lisa
    APPLICANT: Resner, Marshall R
    TITLE OF INVENTION: POLY-ACETYL GLUCOSAMINE. (PNAG/dPNAG)-BINDING
    TITLE OF INVENTION: POLY-N-ACETYL GLUCOSAMINE. (PNAG/dPNAG)-FILE REFERENCE: B0801.70300US01
    TITLE OF INVENTION: PEPTIDES AND METHODS OF USE THEREOF
    FILE REFERENCE: B0801.70300US01
    FILE REFERENCE: 2004-04-11
    PRIOR FILING DATE: 2004-04-11
    PRIOR FILING DATE: 2004-04-11
    PRIOR FILING DATE: 2004-04-11
    NUMBER OF SEQ ID NOS: 61
    SOFTWARE: Patentin version 3.3
    SEQ ID NO 1
    LENGTH: 124
    TYPE: PRT
    ORGANISM: Homo sapiens
    US-11-111-688-1
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69.4%; Score 59; DB 7; Length 124;
Best Local Similarity 55.0%; Pred. No. 0.0037;
Matches 11; Conservative 1; Mismatches 8; Indels
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PRIOR APPLICATION NUMBER: 60/615284
PRIOR FILING DATE: 2004-10-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 116
TYPE: PRT
ORGANISM: Homo sapiens
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Search completed: October 18, 2006, 20:58:14 Job time : 14.3299 secs

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Sequence 1, Application PC/TUS9604206 GENERAL INFORMATION:
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                                                                                                                                                           ; Search time 294.33 Seconds (without alignments) 103.758 Million cell updates/sec
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2: FEMC_Celerra_SIDS3/ptcdata/2/paa/USO66_COMB.pep:*

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4: EMC_Celerra_SIDS3/ptcdata/2/paa/USO74_COMB.pep:*

5: FEMC_Celerra_SIDS3/ptcdata/2/paa/USO74_COMB.pep:*

6: FEMC_Celerra_SIDS3/ptcdata/2/paa/USO76_COMB.pep:*

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11: FEMC_Celerra_SIDS3/ptcdata/2/paa/USO87_COMB.pep:*

12: FEMC_Celerra_SIDS3/ptcdata/2/paa/USO87_COMB.pep:*

13: FEMC_Celerra_SIDS3/ptcdata/2/paa/USO87_COMB.pep:*

14: FEMC_Celerra_SIDS3/ptcdata/2/paa/USO87_COMB.pep:*

15: FEMC_Celerra_SIDS3/ptcdata/2/paa/USO87_COMB.pep:*

16: FEMC_Celerra_SIDS3/ptcdata/2/paa/USO87_COMB.pep:*

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18: FEMC_Celerra_SIDS3/ptcdata/2/paa/USO97_COMB.pep:*

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10: FEMC_Celerra_SIDS3/ptcdata/2/paa/USO97_COMB.pep:*

11: FEMC_Celerra_SIDS3/ptcdata/2/paa/USO97_COMB.pep:*

12: FEMC_Celerra_SIDS3/ptcdata/2/paa/USO97_COMB.pep:*

13: FEMC_Celerra_SIDS3/ptcdata/2/paa/USO97_COMB.pep:*

14: FEMC_Celerra_SIDS3/ptcdata/2/paa/USO97_COMB.pep:*

15: FEMC_Celerra_SIDS3/ptcdata/2/paa/USO97_COMB.pep:*

16: FEMC_Celerra_SIDS3/ptcdata/2/paa/USO99_COMB.pep:*

17: FEMC_Celerra_SIDS3/ptcdata/2/paa/USO99_COMB.pep:*

18: FEMC_Celerra_SIDS3/ptcdata/2/paa/USO99_COMB.pep:*

19: FEMC_Celerra_SIDS3/ptcdata/2/paa/USO99_COMB.pep:*

10: FEMC_Celerra_SIDS3/ptcdata/2/paa/USO99_COMB.pep:*

11: FEMC_Celerra_SIDS3/ptcdata/2/paa/USO99_COMB.pep:*

12: FEMC_Celerra_SIDS3/ptcdata/2/paa/USO99_COMB.pep:*

13: FEMC_Celerra_SIDS3/ptcdata/2/paa/USO99_COMB.pep:*

14: FEMC_Celerra_SIDS3/ptcdata/2/paa/USO99_COMB.pep:*
GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
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/paa/US100_(
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/paa/US102_
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'EMC_Celerra_SIDS3/ptodata/
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Maximum Match 100%
Listing first 45 summaries
                                                                                                          - protein search, using sw model
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Celerra_SIDS3/
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Sequence 12, Appl
Sequence 1626, Ap
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102697,
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Sequence 14790,
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Sequence 82
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US-10-620-621-6
US-10-620-621-6
US-10-758-397A-1
US-10-758-397A-1
US-09-791-537-11946
US-09-791-537-14835
US-09-791-537-14835
US-09-791-537-14831
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US-10-293-418-1626
US-11-264-44-1626
US-11-266-444-1626
US-60-725-626-1626
US-60-735-988-1626
US-60-735-988-1626
US-10-961-567A-3
US-10-961-567A-3
US-09-791-537-135207
US-11-202-507A-14
US-11-202-507A-14
US-11-202-507A-14
US-11-202-507A-14
US-09-791-537-135370
US-09-791-537-129898
US-09-791-537-129898
US-09-791-537-129898
US-09-791-537-16277
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US-10-312-316-47
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US-10-620-621-1
US-10-758-397-11
US-10-758-397A-11
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ALIGNMENTS

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Sequence 1, Application US/10468924
GENERAL INFORMATION:
APPLICANT: YEDA Research and Development Co. Ltd
APPLICANT: WOZES, Edna
TITLE OF INVENTION: Synthetic Human Peptides and Pharmaceutical Compositions Compris:
TITLE OF INVENTION: Synthetic Human Peptides and Pharmaceutical Compositions Compris:
FILE REFERENCE: TEVA-003 PCT
CURRENT APPLICATION NUMBER: US/10/468,924
CURRENT FILING DATE: 2003-08-21
PRIOR PILING DATE: 2001-02-26
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                                                                                                                                                                                                                                                                                                                                                                            SYNTHETIC PEPTIDES AND PHARMACEUTICAL COMPOSITIONS COMPRISING THEM FOR THE TREATMENT OF SYSTEMIC LUPUS ERYTHEMATOSUS (SLE)
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                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: SYNTHETIC PEPTIDES AND PHARMACEUTICAL
TITLE OF INVENTION: COMPOSITIONS COMPRISING THEM FOR THE
TITLE OF INVENTION: OF SYSTEMIC LUPUS ERYTHEMATOSUS (SLE)
NUMBER OF SEQUENCES: 10
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/04206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 79; DB 34; Length 20;
Pred. No. 3.6e-06;
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                                                                                         5; Indels
                                          Score 79; DB 1; 1
Pred. No. 3.6e-06;
                                       Query Match 92.9%; Score 79; DB Best Local Similarity 75.0%; Pred. No. 3.6e Matches 15; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                         Sequence 6, Application PC/TUS9604206
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 113,159
FILING DATE: 28-MAR-1995
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                        1 TGÝÝMQWVKQSPEKSLEWIG 20
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SOFTWARE: Patentin version 3.1
SEQ ID NO.1
LENGTH: 20
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: peptide
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
PCT-IL02-00148-1
                                                                                                                                                                                                                                                                                          PCT-US96-04206-6
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US-10-468-924-1
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TITLE OF INVENTION: PARENTERAL FORMULATIONS OF PEPTIDES FOR THE TREATMENT OF SYSTEMIC
TITLE OF INVENTION: ERYTHEMATOSUS
FILE REFERENCE: 2609/68911-A
CURRENT APPLICATION NUMBER: US/10/758,397A
CURRENT PILING DATE: 2004-01-14
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.1
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; Sequence 1 Application PC/TIL0200148
; GENERAL INFORMATION:
; APPLICANT: YEDA Research and Development Co. Ltd
; APPLICANT: WOZES, Edna
; TITLE OF INVENTION: PEPTIDES FROM THE 16/6id ANTIBODY FOR TREATING SLE
; FILE REFERENCE: TEVA-003 POT
; CURRENT APPLICATION NUMBER: PCT/IL02/00148
; CURRENT PILING DATE: 2003-10-15
; PRIOR PILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin version 3.1
; LENGTH: 20
; TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Synthetic peptide based on CDR of mouse autoantibody
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Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 20; Conservative 0; Mismatches 0;
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OTHER INFORMATION: X= Gln, Asp, Glu or Arg
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LOCATION: (5). ...(5)
OTHER INFORMATION: X= Met, Ala or Val
                                                                                                                                                                                      Sequence 11, Application US/10758397A GENERAL INFORMATION:
                        TGYYXXXXQSPEKSLEWIG 20
                                                                   1 TGYYXXXXOSPEKSLEWIG 20
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OTHER INFORMATION: X= Trp or Ala
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INFORMATION: X= Val or Ser
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NAME/KEY: MISC_FEATURE
LOCATION: (6). (6)
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LENGTH: 20
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BLOOMAX: Inc.
APPLICANT: BLOOMAX: Inc.
APPLICANT: BLOOMAX: Inc.
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBIR: TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT PILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PALENTIN VERSION 3.0
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Pred. No. 1.9e-05;
0; Mismatches 5; Indels
     METHODS OF USE THEREOF
TITLE OF INVENTION: METHODS OF USE THEREC FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 14790
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Best Local Similarity 75.0%;
Matches 15; Conservative
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Best Local Similarity 75.0
Matches 15, Conservative
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US-09-791-537-14790
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LENGTH: 112
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APPLICANT: Bionomix, Inc.
APPLICANT: Bolowix, Inc.
APPLICANT: Debe, Derek
TITLE OF INVENTION: WETHODS OF USE THEREOF
TITLE OF INVENTION: MEMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARKE: PATCHIN VERSION 3.0
SEQ ID NO 11946
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APPLICANT: Debc, Derek
APPLICANT: Debc, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION WIMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version: 3.0
SEQ ID NO 82724
LENGTH: 105
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GENERAL INFORMATION:
APPLICANT: Bionomix, inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
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        Indels
        2,
     0; Mismatches
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GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
                                                      1 TGYYXXXXQSPEKSLEWIG 20
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Matches 15; Conservative
     15; Conservative
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CORGANISM: Mus musculus
US-09-791-537-11946
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US-09-791-537-82724 ·
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US-09-791-537-14790
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November 2005

generate two sets of results each. The Published_Applications databases have been split into two parts to Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches. Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases. Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions .rnpbm (Published_Applications_NA_Main) and .rnpbn (Published_Applications_NA_New).
Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions .rapbm (Published_Applications_AA_Main) and .rapbn (Published_Applications_AA_New).

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Search completed: October 18, 2006, 20:55:48
Job time : 80.3814 secs
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LENGTH: 129
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Sequence 7, Application US/11202507A

Sequence 7, Application No. US20060057111A1

GENERAL INFORMATION:

APPLICANT: Hedlund, Gunnar

APPLICANT: Wallen-Ohman, Marie

TITLE OF INVENTION: COMBINATION WITH ANOTHER ANTICANCER AGENT

TITLE OF INVENTION: COMBINATION WITH ANOTHER ANTICANCER AGENT

TITLE OF INVENTION: UNBER: US/11/202,507A

CURRENT APPLICATION NUMBER: US/11/202,507A

CURRENT APPLICATION NUMBER: US/11/202,507A

MUMBER OF SEQ ID NOS: 16

SOFTWARE PALENT APPLICATION NUMBER: 2004-08-13

NUMBER OF SEQ ID NOS: 16

SEQ ID NO 7

LENGTH: 672
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Sequence 1, Application US/09900766
Sequence 1, Application US/09000766
Sublication No. US20030039655A1
GENERAL INFORMATION:
APPLICANT: FORSBERG, GORAN
APPLICANT: ANTONSSON, BVA
APPLICANT: WALSE, BJORN
TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
FILE REPERENCE: POLIBBUSO;10104199
CURRENT APPLICATION NUMBER: US/09/900,766
CURRENT FILING DATE: 2001-07-06
NUMBER OF SEQ ID NOS: 7
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0
                                      Score 68; DB 6; Length 671;
Pred. No. 0.0072;
0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 80.0%; Score 68; DB 3; Length 672; 11 Similarity 65.0%; Pred. No. 0.0072; 13; Conservative 0; Mismatches 7: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAMES/KEY: PEPTIDE
LOCATION: (1)..(672)
OTHER INFORMATION: Conjugate protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Conjugate Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TGYYXXXXQSPEKSLEWIG 20
                                                                                                                              1 TGYYXXXXXQSPEKSLEWIG 20
                                                                                                                                                                       30 TGYYMHWVKQSPGKGLEWIG 49
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LOCATION: (449)..(672)
OTHER INFORMATION: Light Chain
                                      ch 80.0%;
1 Similarity 65.0%;
13; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin version 3.0 SEQ ID NO 1 LENGTH: 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
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                                        Query Match
Best Local Similarity
Matches 13; Conserva
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Matches 13; Conserv
US-11-202-507A-14
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US-11-202-507A-7
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APPLICANT: Shelton, David L.
TITLE OF INVENTION: AGONIST ANTI-TRK-C MONOCLONAL ANTIBODIES
TITLE OF INVENTION: AGONIST ANTI-TRK-C MONOCLONAL ANTIBODIES
CURRENT APPLICATION NUMBER: US/10/312,316
CURRENT PILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: 60/238,319
PRIOR FILING DATE: 2000-10-05
RINNBER OF SEQ ID NOS: 89
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 65; DB 4; Length 129;
Pred. No. 0.0045;
0; Mismatches 7; Indels
Length 672;
  Query Match 80.0%; Score 68; DB 6; Length 672 Best Local Similarity 65.0%; Pred. No. 0.0072; Matches 13; Conservative 0; Mismatches 7; Indels
                                                                                                                                                                                                                    RESULT 15
US-10-312-316-47
is Sequence 47, Application US/10312316
ipublication No. US20040137513A1
igenERAL INFORMATION:
                                                                                                 1 TGYYXXXXQSPEKSLEWIG 20
                                                                                                                                              30 TGYYMHWVKQSPGKGLEWIG 49
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63.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 76.5
Best Local Similarity 63.2
Matches 12; Conservative
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; ORGANISM: Homo sapiens
US-10-312-316-47
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Sequence 14, Application US/11202507A
Publication No. US20060057111A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hollund, Gunnar
APPLICANT: Porsberg, Goran
APPLICANT: Wallen-Ohman, Marie
TITLE OF INVENTION: COMBINATION WITH ANOTHER ANTICANCER AGENT
FILE REPERENCE: P03024US1
CURRENT APPLICATION NUMBER: US/11/202,507A
CURRENT PILING DATE: 2005-08-12
CURRENT PILING DATE: 2006-08-13
PRIOR FILING DATE: 2004-08-13
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APPLICANT: JUNE-KUNKEI, Maria
APPLICANT: Gardian
FILE REFERENCE: 10060 NP
CURRENT FILING NUMBER: US/10/961,567A
CURRENT FILING DATE: 2004-10-08
PRIOR FILING DATE: 2003-10-10
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.2
SEQ ID NO 9
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                                                                                                                                                                                                                  Length 467;
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Pred. No. 0.0015;
1; Mismatches 6; Indels
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                                                                                                                       ; FEATURE:
; OTHER INFORMATION: pD17-20H4.9.h4a amino acid sequence
US-10-961-567A-3
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; OTHER INFORMATION: 20H4.9-IgG1 amino acid sequence
US-10-961-567A-9
                                                                                                                                                                                                             Query Match
83.5%; Score 71; DB 5; Le
Best Local Similarity 65.0%; Pred. No. 0.0015;
Matches 13; Conservative 1; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/10961567A Publication No. US20050095244A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                               1 TGYYXXXXQSPEKSLEWIG 20
                                                                                                                                                                                                                                                                                                                                                        49 SGYYWSWIROSPEKGLEWIG 68
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SOFTWARE: PatentIn version 3.2 SEQ ID NO 3 LENGTH: 467 TYPE: PRT ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 65.0%;
Matches 13; Conservative
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SOFTWARE: Patentin version 3.3
SEQ ID NO 14
LENGTH: 671
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-11-202-507A-14
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Sequence 1626, Application US/11266444

Publication No. US20060062789A1

GENERAL INFORMATION:

APPLICAMT: Nuben et al.

TILE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulate

TILE REFERENCE: PF523P1D1

CURRENT APPLICATION NUMBER: US/11/266,444

FILE REFERENCE: PF523P1D1

CURRENT APPLICATION NUMBER: 09/800,746

PRIOR PILING DATE: 2001-06-15

PRIOR FILING DATE: 2000-06-16

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2000-103-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-25

NUMBER: OF SEQ ID NOS: 3229

SEQ ID NO 1626

LENGTH: 255

LENGTH: 255
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                          Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 3247 SEQ ID NO 1626 LENGTH: 255
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APPLICANT: Une-Kunkel, Maria
APPLICANT: Santoro, Marc
CURRENT: FULLY HUMAN ANTIBODIES AGAINST HUMAN 4-1BB
FILE REFERENCE: 10066 NP
CURRENT APPLICATION NUMBER: US/10/961,567A
CURRENT FILING DATE: 2004-10-08
PRIOR FILING DATE: 2003-10-10
NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                             83.5%; Score 71; DB 6; Length 255; ilarity 65.0%; Pred. No. 0.00083; Conservative 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 6; Length 255;
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65.0%; Pred. No. 0.00083;
tive 1; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                 1 TGYYXXXXXQSPEKSLEWIG 20
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                                                                                                                                                                                                                                                                                                                                                           30 SGYYWSWVRQSPEKGLEWIG 49
    PRIOR FILING DATE: 2000-10-17
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Best Local Similarity 65.0°
Matches 13; Conservative
                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-1626
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; ORGANISM: Homo sapiens
US-11-266-444-1626
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Best Local Similarity
Matches 13; Conserv
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Gaps
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS.

FILE REPERENCE: PF23783

CURRENT APPLICATION NUMBER: US/11/054,515

FRIOR APPLICATION NUMBER: 06/543,296

PRIOR FILING DATE: 2005-02-11

PRIOR PILING DATE: 2004-06-18

PRIOR PILING DATE: 2004-06-18

PRIOR PILING DATE: 2004-06-18

PRIOR PILING DATE: 2004-06-18

PRIOR PILING DATE: 2004-06-14

PRIOR PILING DATE: 2001-11-16

PRIOR PILING DATE: 2001-11-16

PRIOR PILING DATE: 2001-12-19

PRIOR PILING DATE: 2001-12-19

PRIOR PILING DATE: 2001-06-15

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-31

PRIOR PILING DATE: 2001-03-31

PRIOR PILING DATE: 2001-03-316

PRIOR PILING DATE: 2001-03-316

PRIOR PILING DATE: 2001-03-316

PRIOR PILING DATE: 2001-03-316

PRIOR PPLICATION NUMBER: 60/240,816
                                                                                                                                                                                    APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REPERENCE: P523P2
CURRENT APPLICATION: MUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-6
PRIOR FILING DATE: 2001-12-19
PRIOR FILING DATE: 2001-12-19
PRIOR FILING DATE: 2001-6-15
PRIOR PILING DATE: 2001-6-15
PRIOR PILING DATE: 2001-06-15
PRIOR PILING DATE: 2001-06-15
PRIOR PILING DATE: 2001-06-15
PRIOR PILING DATE: 2001-06-15
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-31
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2000-06-16
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Pred. No. 0.00083;
1; Mismatches 6; Indels
                                                                                                          Sequence 1626, Application US/10293418
Publication No. US20030223996A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 1626, Application US/11054515; Publication No. US20050255532A1; GENERAL INFORMATION;
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il Similarity 65.0%;
13; Conservative 1
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Best Local Similarity
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US-11-054-515-1626
                                                                                      JS-10-293-418-1626
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TITLE OF INVENTION: PARENTERAL FORMULATIONS OF PEPTIDES FOR THE TREATMENT OF SYSTEMIC
TITLE OF INVENTION: ERYTHEMATOSUS
FILE REPERENCE: 2609/68811-A
CURRENT APPLICATION NUMBER: US/10/758,397
CURRENT FILING DATE: 2004-01-14
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.1
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| Sequence 1626, Application US/09880748
| Publication No. US2003005937A1
| GENERAL INFORMATION:
| APPLICANT: Ruben et al. |
| TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS FILE REFERENCE: PF523
| CURRENT APPLICATION NUMBER: US/09/880,748
| CURRENT FILING DATE: 2000-06-15
| PRIOR FILING DATE: 2000-06-15
| PRIOR FILING DATE: 2000-06-15
| PRIOR FILING DATE: 2000-10-17
| PRIOR FILING DATE: 2001-03-21
| PRIOR FILING DATE: 2001-05-25
| NUMBER OF SEQ ID NOS: 3239
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65.0%; Pred. No. 0.00083;
tive 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92.9%; Score 79; DB 5; Length 20; 75.0%; Pred. No. 2.7e-06; Live 0; Mismatches 5; Indels
                               Indels
l Similarity 75.0%; Pred. No. 2.7e-06;
15; Conservative 0; Mismatches 5;
                                                                                   1 TGYYXXXXXQSPEKSLEWIG 20
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                                                                                                                                                                                                                                                                       ; Sequence 1, Application US/10758397; Publication No. US20050008634A1; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Matches 13; Conservative
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US-09-880-748-1626
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US-10-758-397-1
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